

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 20:26:59 ; Search time 189 Seconds
 (without alignments)

US-10-727-358-5
 US-10-727-358-5
 US-09-560-385A-13

Perfect score: 18
 Sequence: cggacccataggccaag 18

Scoring table: IDENTITY_NUC
 GapOp 10.0 , GapExt: 1.0

Searched: 1303057 seqs, 888788028 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 300 summaries

Database : Issued Patents NA,*

1: /cgn2_6/ptodata/1/ina/1-COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5-COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A-COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B-COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H-COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PP-COMB.seq:*

7: /cgn2_6/ptodata/1/ina/RB-COMB.seq:*

8: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	18	100.0	4094	2	US-08-571-758-5	Sequence 5, Appli	c
2	18	100.0	4094	2	US-08-909-984A-5	Sequence 5, Appli	c
3	18	100.0	4094	2	US-08-909-983-5	Sequence 5, Appli	c
4	15.4	85.6	543	3	US-09-621-975-17349	Sequence 17349, A	c
5	15.4	85.6	29889	3	US-09-949-016-13682	Sequence 13682, A	c
6	15.4	85.6	97195	3	US-09-949-016-12212	Sequence 12212, A	c
7	15.4	85.6	83.3	3	US-10-131-827-75899	Sequence 75899, A	c
8	15	83.3	163	3	US-03-511-999C-28900	Sequence 28900, A	c
9	15	83.3	783	3	US-09-157-910-6	Sequence 6, Appli	c
10	15	83.3	868	3	US-08-909-937-159	Sequence 159, Appli	c
11	15	83.3	2399	3	US-09-021-655-508	Sequence 508, Appli	c
12	15	82.2	601	3	US-09-949-016-23074	Sequence 23074, A	c
13	14.8	82.2	601	3	US-09-949-016-169781	Sequence 169781, A	c
14	14.8	82.2	2846	2	US-08-571-758-7	Sequence 7589, A	c
15	14.8	82.2	2846	2	US-08-909-984A-7	Sequence 7, Appli	c
16	14.8	82.2	2846	2	US-08-909-984A-7	Sequence 7, Appli	c
17	14.8	82.2	2846	2	US-08-909-984A-7	Sequence 7, Appli	c
18	14.8	82.2	3469	3	US-09-560-388A-23	Sequence 23, Appli	c
19	14.8	82.2	3511	3	US-09-560-385A-19	Sequence 19, Appli	c
20	14.8	82.2	3585	3	US-09-560-385A-21	Sequence 21, Appli	c
21	14.8	82.2	3621	3	US-09-560-385A-17	Sequence 17, Appli	c
22	14.8	82.2	3759	3	US-09-560-385A-15	Sequence 15, Appli	c
23	14.8	82.2	3930	3	US-09-560-385A-13	Sequence 13, Appli	c
24	14.8	82.2	3931	2	US-09-270-767-6755	Sequence 1, Appli	c
25	14.8	82.2	3931	3	US-10-841-139-1	Sequence 1, Appli	c
26	14.8	82.2	3931	3	US-09-876-176-1	Sequence 1, Appli	c
27	14.8	82.2	4108	3	US-09-919-172-15	Sequence 1, Appli	c
28	14.8	82.2	17410	2	US-07-841-646-3	Sequence 3, Appli	c
29	14.8	82.2	17410	2	US-08-177-023-3	Sequence 3, Appli	c
30	14.8	82.2	17410	2	US-08-447-570-3	Sequence 3, Appli	c
31	14.8	82.2	17410	2	US-08-449-700-3	Sequence 3, Appli	c
32	14.8	82.2	17410	2	US-08-449-699-3	Sequence 3, Appli	c
33	14.8	82.2	17410	3	US-09-188-925-3	Sequence 3, Appli	c
34	14.8	82.2	17410	3	US-08-957-425-3	Sequence 3, Appli	c
35	14.8	82.2	17410	3	US-10-311-799-3	Sequence 3, Appli	c
36	14.8	82.2	17410	3	US-09-513-99C-264-39	Sequence 3, Appli	c
37	14.8	82.2	17415	3	US-09-423-821B-1	Sequence 402, App	c
38	14.8	82.2	17415	6	PCT-US95-07349-1	Sequence 402, App	c
39	14.8	82.2	9798	3	US-09-949-016-11990	Sequence 403, App	c
40	14.8	82.2	9798	3	US-09-949-016-16518	Sequence 403, App	c
41	14.8	82.2	9798	3	US-09-949-016-16518	Sequence 403, App	c
42	14.8	80.0	364	3	US-09-513-99C-264-39	Sequence 26439, A	c
43	14.8	80.0	658	3	US-09-611-638-402	Sequence 402, App	c
44	14.4	80.0	8323	2	US-08-866-642-8	Sequence 402, App	c
45	14.4	80.0	939	3	US-09-641-630-403	Sequence 402, App	c
46	14.4	80.0	1022	3	US-09-557-584-5	Sequence 403, App	c
47	14.4	80.0	1022	3	US-10-104-041-327	Sequence 403, App	c
48	14.4	80.0	3153	3	US-08-110-300A-8	Sequence 403, App	c
49	14.4	80.0	8323	2	US-08-110-300A-8	Sequence 403, App	c
50	14.4	80.0	10367	6	PCT-US93-08041-9	Sequence 403, App	c
51	14.4	80.0	18433	3	US-09-433-322B-2	Sequence 403, App	c
52	14.4	80.0	8323	3	US-09-597-2	Sequence 403, App	c
53	14.4	80.0	8323	6	PCT-US93-08041-8	Sequence 403, App	c
54	14.4	80.0	10367	2	US-08-10-300A-9	Sequence 403, App	c
55	14.4	80.0	10367	2	US-08-198-422A-583	Sequence 403, App	c
56	14.4	80.0	10367	6	PCT-US93-08041-9	Sequence 403, App	c
57	14.4	80.0	18433	3	US-09-918-294-6	Sequence 403, App	c
58	14	77.8	459	3	US-09-513-99C-24323	Sequence 21175, A	c
59	14	77.8	5706	3	US-09-270-767-12590	Sequence 12590, A	c
60	14	77.8	2105	3	US-09-949-016-15722	Sequence 15722, A	c
61	14	77.8	197496	10	US-09-949-016-1712-10	Sequence 10, Appli	c
62	13.8	76.7	20	3	US-09-198-422A-583	Sequence 5583, Ap	c
63	13.8	76.7	235	3	US-09-913-99C-21784	Sequence 17184, A	c
64	13.8	76.7	302	2	US-08-849-701-3	Sequence 3, Appli	c
65	13.8	76.7	459	3	US-09-513-99C-24323	Sequence 24323, A	c
66	13.8	76.7	601	3	US-09-949-016-2019	Sequence 2019, A	c
67	13.8	76.7	601	3	US-09-949-016-20120	Sequence 20120, A	c
68	13.8	76.7	601	3	US-09-949-016-21950	Sequence 21950, A	c
69	13.8	76.7	601	3	US-09-949-016-27775	Sequence 27175, A	c
70	13.8	76.7	601	3	US-09-949-016-32556	Sequence 32556, A	c
71	13.8	76.7	601	3	US-09-949-016-32557	Sequence 32557, A	c
72	13.8	76.7	601	3	US-09-949-016-43036	Sequence 43036, A	c
73	13.8	76.7	601	3	US-09-949-016-43037	Sequence 43037, A	c
74	13.8	76.7	601	3	US-09-949-016-46328	Sequence 46928, A	c
75	13.8	76.7	601	3	US-09-949-016-55792	Sequence 55792, A	c
76	13.8	76.7	601	3	US-09-949-016-84271	Sequence 84271, A	c
77	13.8	76.7	601	3	US-09-949-016-86103	Sequence 86103, A	c
78	13.8	76.7	601	3	US-09-949-016-87274	Sequence 87274, A	c
79	13.8	76.7	601	3	US-09-949-016-10128	Sequence 104128, A	c
80	13.8	76.7	601	3	US-09-949-016-10419	Sequence 104129, A	c
81	13.8	76.7	601	3	US-09-949-016-12182	Sequence 127822, A	c
82	13.8	76.7	601	3	US-09-949-016-128159	Sequence 128159, A	c
83	13.8	76.7	601	3	US-09-949-016-142939	Sequence 142939, A	c
84	13.8	76.7	601	3	US-09-949-016-153359	Sequence 153359, A	c
85	13.8	76.7	601	3	US-09-949-016-153360	Sequence 153360, A	c
86	13.8	76.7	601	3	US-09-949-016-167466	Sequence 167466, A	c
87	13.8	76.7	601	3	US-09-949-016-177418	Sequence 177418, A	c
88	13.8	76.7	601	3	US-09-949-016-182373	Sequence 182373, A	c
89	13.8	76.7	601	3	US-09-949-016-182899	Sequence 182899, A	c
90	13.8	76.7	601	3	US-09-949-016-182900	Sequence 182900, A	c
91	13.8	76.7	601	3	US-09-949-016-182901	Sequence 182901, A	c
92	13.8	76.7	601	3	US-09-949-016-182901	Sequence 182901, A	c
93	13.8	76.7	604	3	US-09-97-774-528-233	Sequence 22037, A	c
94	13.8	76.7	604	3	US-10-120-988-233	Sequence 22037, A	c
95	13.8	76.7	616	3	US-09-465-558-15	Sequence 6755, Ap	c
96	13.8	76.7	629	3	US-09-270-767-6755	Sequence 6755, Ap	c
97	13.8	76.7	629	3	US-09-270-767-6755	Sequence 6755, Ap	c

98	13.8	76.7	76.3	3	US-09-586-106-138	Sequence 138, App	c 171	13.8	76.7	44120	3	US-09-949-016-14154
99	13.8	76.7	763	3	US-10-799-870-138	Sequence 138, App	c 172	13.8	76.7	44120	3	US-09-949-016-14155
100	13.8	76.7	792	3	US-03-869-588-26	Sequence 26, App	c 173	13.8	76.7	44120	3	US-09-949-016-14156
101	13.8	76.7	818	3	US-03-030-607-27	Sequence 27, App	c 174	13.8	76.7	44676	3	US-09-949-016-15151
102	13.8	76.7	819	3	US-03-030-607-27	Sequence 27, App	c 175	13.8	76.7	51967	3	US-09-949-016-16982
103	13.8	76.7	818	3	US-03-439-313-27	Sequence 27, App	c 176	13.8	76.7	53336	3	US-09-949-016-12500
104	13.8	76.7	818	3	US-03-352-616A-27	Sequence 27, App	c 177	13.8	76.7	53337	3	US-09-949-016-16092
105	13.8	76.7	818	3	US-03-22-149A-27	Sequence 27, App	c 178	13.8	76.7	53328	3	US-09-949-016-12747
106	13.8	76.7	818	3	US-03-159-812-27	Sequence 27, App	c 179	13.8	76.7	55330	3	US-09-949-016-17146
107	13.8	76.7	818	3	US-03-636-215-27	Sequence 27, App	c 180	13.8	76.7	56448	3	US-09-949-016-19463
108	13.8	76.7	818	3	US-09-685-166A-27	Sequence 27, App	c 181	13.8	76.7	66313	3	US-09-949-016-18803
109	13.8	76.7	818	3	US-03-115-453-27	Sequence 27, App	c 182	13.8	76.7	66213	3	US-09-949-016-16739
110	13.8	76.7	818	3	US-03-688-489-27	Sequence 27, App	c 183	13.8	76.7	63924	3	US-09-949-016-15367
111	13.8	76.7	818	3	US-03-679-426-27	Sequence 27, App	c 184	13.8	76.7	70308	3	US-09-949-016-15601
112	13.8	76.7	818	3	US-03-759-143-27	Sequence 27, App	c 185	13.8	76.7	72742	3	US-09-949-016-16161
113	13.8	76.7	818	3	US-03-651-236-27	Sequence 27, App	c 186	13.8	76.7	83349	3	US-09-949-016-17149
114	13.8	76.7	818	3	US-03-030-606-27	Sequence 27, App	c 187	13.8	76.7	87734	3	US-09-949-016-17521
115	13.8	76.7	818	3	US-03-657-279-27	Sequence 27, App	c 188	13.8	76.7	87752	3	US-09-949-016-18809
116	13.8	76.7	818	3	US-03-012-896-27	Sequence 27, App	c 189	13.8	76.7	91933	3	US-09-949-016-18855
117	13.8	76.7	1088	3	US-10-087-167-107	Sequence 56, App	c 190	13.8	76.7	91933	3	US-09-949-016-18628
118	13.8	76.7	1206	3	US-03-465-558-53	Sequence 53, App	c 191	13.8	76.7	93648	3	US-09-949-016-13139
119	13.8	76.7	1351	2	US-03-07-816-283-5	Sequence 53, App	c 192	13.8	76.7	10790	3	US-09-949-016-800B-2
120	13.8	76.7	1351	2	US-03-417-103-5	Sequence 53, App	c 193	13.8	76.7	103750	3	US-09-949-016-13319
121	13.8	76.7	1351	3	US-03-016-434-1303	Sequence 1303, App	c 194	13.8	76.7	87752	3	US-09-949-016-18809
122	13.8	76.7	1457	3	US-03-596-554-554	Sequence 554, App	c 195	13.8	76.7	91933	3	US-09-949-016-17567
123	13.8	76.7	1559	3	US-03-482-273-56	Sequence 56, App	c 196	13.8	76.7	91933	3	US-09-949-016-18628
124	13.8	76.7	1568	3	US-03-220-132-91	Sequence 91, App	c 197	13.8	76.7	91814	3	US-09-949-016-16205
125	13.8	76.7	1773	3	US-03-495-050-51	Sequence 1067, App	c 198	13.8	76.7	10667	3	US-09-949-016-855A-32
126	13.8	76.7	1847	3	US-03-675-885-4	Sequence 4, App	c 199	13.8	76.7	103750	3	US-09-949-016-17202
127	13.8	76.7	1901	3	US-03-104-047-1811	Sequence 1811, App	c 200	13.8	76.7	109025	3	US-09-949-016-18069
128	13.8	76.7	1943	3	US-03-10-104-1484	Sequence 184, App	c 201	13.8	76.7	109025	3	US-09-949-016-17234
129	13.8	76.7	1970	3	US-10-081-885A-6	Sequence 6, App	c 202	13.8	76.7	10243	3	US-09-949-016-13698
130	13.8	76.7	2325	3	US-10-104-047-242	Sequence 242, App	c 203	13.8	76.7	11814	3	US-09-949-016-16205
131	13.8	76.7	2480	3	US-03-022-655-1096	Sequence 1096, App	c 204	13.8	76.7	11067	3	US-09-949-016-1880
132	13.8	76.7	2871	3	US-03-949-87-111	Sequence 111, App	c 205	13.8	76.7	128863	3	US-09-949-016-1880
133	13.8	76.7	3299	3	US-03-483-376-1	Sequence 275, App	c 206	13.8	76.7	134008	3	US-09-949-016-1880
134	13.8	76.7	3437	3	US-03-929-769-3	Sequence 3, App	c 207	13.8	76.7	135010	3	US-09-949-016-17234
135	13.8	76.7	3437	3	US-10-033-301-21	Sequence 21, App	c 208	13.8	76.7	147840	3	US-09-949-016-18236
136	13.8	76.7	4078	3	US-03-016-434-1154	Sequence 1154, App	c 209	13.8	76.7	14170	3	US-09-949-016-14810
137	13.8	76.7	4719	3	US-03-620-312D-349	Sequence 349, App	c 210	13.8	76.7	205044	3	US-09-949-016-15952
138	13.8	76.7	4541	3	US-03-949-002-258	Sequence 58, App	c 211	13.8	76.7	205044	3	US-09-949-016-15953
139	13.8	76.7	6386	2	US-03-483-376-1	Sequence 1, App	c 212	13.8	76.7	174318	3	US-09-949-016-1812
140	13.8	76.7	7240	3	US-03-95-795A-1	Sequence 1, App	c 213	13.8	76.7	174318	3	US-09-949-016-14913
141	13.8	76.7	7883	3	US-03-949-016-13183	Sequence 13183, App	c 214	13.8	76.7	174318	3	US-09-949-016-17294
142	13.8	76.7	9811	3	US-03-949-016-12759	Sequence 12759, App	c 215	13.8	76.7	217290	3	US-09-949-016-12980
143	13.8	76.7	10625	3	US-03-949-016-16310	Sequence 16310, App	c 216	13.8	76.7	217290	3	US-09-949-016-12201
144	13.8	76.7	12470	3	US-03-949-002-2847	Sequence 847, App	c 217	13.8	76.7	217290	3	US-09-949-016-13363
145	13.8	76.7	14753	3	US-03-821-736-3	Sequence 1505, App	c 218	13.8	76.7	246340	2	US-08-724-394A-21
146	13.8	76.7	16356	3	US-03-949-016-15505	Sequence 1505, App	c 219	13.8	76.7	246340	2	US-08-724-394A-22
147	13.8	76.7	16716	3	US-03-949-016-17050	Sequence 17060, App	c 220	13.8	76.7	246344	3	US-09-949-016-13113
148	13.8	76.7	18037	3	US-03-949-016-13678	Sequence 13678, App	c 221	13.8	76.7	265038	3	US-09-949-016-15779
149	13.8	76.7	25458	3	US-03-949-016-13986	Sequence 13986, App	c 222	13.8	76.7	300402	3	US-09-949-016-15362
150	13.8	76.7	28721	3	US-03-949-002-622	Sequence 622, App	c 223	13.8	76.7	30533	3	US-09-949-016-15371
151	13.8	76.7	28162	3	US-03-949-016-17319	Sequence 17319, App	c 224	13.8	76.7	30533	3	US-09-949-016-15372
152	13.8	76.7	25175	3	US-03-949-016-16247	Sequence 16247, App	c 225	13.8	76.7	422592	3	US-09-949-016-14182
153	13.8	76.7	25175	3	US-03-949-016-16248	Sequence 16248, App	c 226	13.8	76.7	45924	3	US-09-949-016-12896
154	13.8	76.7	30569	3	US-03-949-016-12592	Sequence 16273, App	c 227	13.8	76.7	451925	3	US-09-949-016-17305
155	13.8	76.7	25458	3	US-03-949-016-13986	Sequence 13986, App	c 228	13.8	76.7	45526	3	US-09-949-016-14157
156	13.8	76.7	27271	3	US-03-949-002-622	Sequence 622, App	c 229	13.8	76.7	481115	3	US-09-949-016-11940
157	13.8	76.7	27284	3	US-03-949-016-15417	Sequence 15417, App	c 230	13.8	76.7	1230205	3	US-09-194-016-194A-1
158	13.8	76.7	28550	3	US-03-949-016-13106	Sequence 13106, App	c 231	13.8	76.7	1230203	3	US-09-438-185A-1
159	13.8	76.7	30569	3	US-03-949-016-12410	Sequence 12729, App	c 232	13.8	76.7	312	3	US-09-113-999C-35050
160	13.8	76.7	30569	3	US-03-949-016-12410	Sequence 12729, App	c 233	13.8	76.7	491	3	US-09-513-999C-32209
161	13.8	76.7	30569	3	US-03-949-016-12410	Sequence 12729, App	c 234	13.8	76.7	530	3	US-09-661-325-28
162	13.8	76.7	31208	3	US-03-852-057-3	Sequence 3, App	c 235	13.8	76.7	530	3	US-10-012-522-28
163	13.8	76.7	32782	3	US-03-949-016-12382	Sequence 12382, App	c 236	13.8	76.7	601	3	US-09-949-016-25393
164	13.8	76.7	38772	3	US-03-949-016-12729	Sequence 12729, App	c 238	13.8	76.7	601	3	US-09-949-016-5261
165	13.8	76.7	39498	3	US-03-949-016-12410	Sequence 12410, App	c 239	13.8	76.7	601	3	US-09-949-016-88950
166	13.8	76.7	39498	3	US-03-949-016-16505	Sequence 16505, App	c 240	13.8	76.7	601	3	US-09-949-016-12252
167	13.8	76.7	44120	3	US-03-949-016-14151	Sequence 14151, App	c 241	13.8	76.7	601	3	US-09-949-016-15498
168	13.8	76.7	44120	3	US-03-949-016-14153	Sequence 14153, App	c 242	13.8	76.7	601	3	US-09-949-016-18054
169	13.8	76.7	44120	3	US-03-949-016-14153	Sequence 14153, App	c 243	13.8	76.7	658	3	US-09-533-559-6647

RESULT 1
 US-08-571-758-5
 ; Sequence 5, Application US/08571758
 ; Patente No. 570675
 ; GENERAL INFORMATION:
 ; APPLICANT: Rubin, Gerry M.
 ; APPLICANT: Therrien, Marc
 ; APPLICANT: Chang, Henry C.
 ; APPLICANT: Karim, Felix D.
 ; APPLICANT: Wasserman, David A.
 ; TITLE OF INVENTION: A No. 574275el Protein Kinase Required for Ras

ALIGNMENTS

RESULT 1
 US-08-571-758-5
 ; Sequence 5, Application US/08571758
 ; Patente No. 570675
 ; GENERAL INFORMATION:
 ; APPLICANT: Rubin, Gerry M.
 ; APPLICANT: Therrien, Marc
 ; APPLICANT: Chang, Henry C.
 ; APPLICANT: Karim, Felix D.
 ; APPLICANT: Wasserman, David A.
 ; TITLE OF INVENTION: A No. 574275el Protein Kinase Required for Ras

RESULT 2
 US-08-909-994A-5
 ; Sequence 5, Application US/08909984A
 ; Patent No. 5747275
 ; GENERAL INFORMATION:
 ; APPLICANT: Rubin, Gerry M.
 ; APPLICANT: Therrien, Marc
 ; APPLICANT: Chang, Henry C.
 ; APPLICANT: Karim, Felix D.
 ; APPLICANT: Wasserman, David A.
 ; TITLE OF INVENTION: A No. 574275el Protein Kinase Required for Ras
 ; TITLE OF INVENTION: Signal Transduction
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/909,984A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B96-010
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4094 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-571-758-5

SEQUENCE ALIGNMENT

Sequence 62, APL1
 Sequence 62, APL1
 Sequence 46, APL1
 Sequence 1995, APL1
 Sequence 45, APL1
 Sequence 6, APL1
 Sequence 1237, APL1
 Sequence 344, APL1
 Sequence 12381, APL1
 Sequence 13791, APL1
 Sequence 17225, APL1
 Sequence 14710, APL1
 Sequence 15394, APL1
 Sequence 17291, APL1
 Sequence 12806, APL1
 Sequence 15767, APL1
 Sequence 12879, APL1
 Sequence 16841, APL1
 Sequence 12826, APL1
 Sequence 17062, APL1
 Sequence 12653, APL1
 Sequence 15395, APL1
 Sequence 14319, APL1
 Sequence 16821, APL1
 Sequence 1, APL1
 Sequence 1, APL1
 Sequence 13191, APL1
 Sequence 1, APL1
 Sequence 15568, APL1
 Sequence 17433, APL1
 Sequence 15548, APL1
 Sequence 38, APL1
 Sequence 12544, APL1
 Sequence 15517, APL1
 Sequence 15238, APL1
 Sequence 11989, APL1
 Sequence 17130, APL1
 Sequence 14264, APL1
 Sequence 15999, APL1
 Sequence 12876, APL1
 Sequence 13266, APL1
 Sequence 13266, APL1
 Sequence 13546, APL1
 Sequence 12111, APL1
 Sequence 15940, APL1
 Sequence 12268, APL1
 Sequence 15725, APL1
 Sequence 16397, APL1
 Sequence 14577, APL1
 Sequence 14578, APL1
 Sequence 9726, APL1
 Sequence 1222, APL1
 Sequence 4036, APL1
 Sequence 5910, APL1
 Sequence 21192, APL1
 Sequence 10057, APL1
 Sequence 4092, APL1

NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: B96-010
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4094 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-909-984A-5

Query Match Best local Similarity 100.0%; Score 18; DB 2; Length 4094;
 Best Local Similarity 100.0%; Pred. No. 5.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CGGACCCCTAGAGGCAAG 18
 Db 295 295 CGGACCCCTAGAGGCAAG 313

RESULT 3

US-08-909-983-5

; Sequence 5, Application US/08909983
 GENERAL INFORMATION:
 APPLICANT: Rubin, Gerry M.
 APPLICANT: Therrien, Marc
 APPLICANT: Chang, Henry C.
 APPLICANT: Karim, Felix D.
 APPLICANT: Wasserman, David A.
 TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
 TITLE OF INVENTION: signal transduction
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/909,983
 FILING DATE: 12-JUN-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/571,758
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: B96-010
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-342
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:

LENGTH: 4094 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-909-983-5

RESULT 4

US-09-621-976-17349/c

; Sequence 17349, Application US/09621976
 GENERAL INFORMATION:
 PATENT NO. 6639063
 APPLICANT: Dumaine Edwards, J.B.
 APPLICANT: Giordano, J.Y.
 TITLE OF INVENTION: ESTs and Encoded Human Proteins
 FILE REFERENCE: GENBET-054PR2
 CURRENT APPLICATION NUMBER: US/09/621,976
 CURRENT FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 19335
 SOFTWARE: Patent.pm
 SEQ ID NO 17349
 LENGTH: 543
 TYPE: DNA
 ORGANISM: Homo sapiens

US-09-621-976-17349

RESULT 5

US-09-949-016-13682

; Sequence 13682, Application US/09949016
 PATENT NO. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 13682
 LENGTH: 29889
 TYPE: DNA
 ORGANISM: Human

US-09-949-016-13682

RESULT 6

US-09-949-016-12212/c

Query Match Best local Similarity 85.6%; Score 15.4; DB 3; Length 29889;
 Best Local Similarity 94.1%; Pred. No. 1.5e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GGACCCCTAGAGGCAAG 18
 Db 29541 GGACCCCTAGAGGCAAG 29557

```

; Sequence 12212, Application US/09949016
; Patent No. 612339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; SEQ ID NO 12212
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12212
; LENGTH: 97195
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(97195)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-12212

RESULT 7
US-09-949-016-16971/c
; Sequence 16971, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY APPLICATION NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16971
; LENGTH: 97195
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc-feature
; LOCATION: (1)..(97196)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-16971

Query Match 85.6%; Score 15.4; DB 3; Length 97195;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACCTTAGGGCAAG 18
Db 77970 GGACCTTAGGGCAAG 77954

RESULT 8
US-10-131-827-7589
; Sequence 7589, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIORITY APPLICATION NUMBER: 60/296,764
; PRIORITY FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7589
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-7589

Query Match 83.3%; Score 15; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GGACCTTAGGGCA 15
Db 18 GGACCTAGGGCA 32

RESULT 9
US-09-513-999C-28900
; Sequence 28900, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIORITY APPLICATION NUMBER: US 60/122,487
; PRIORITY FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: PatentIn
; SEQ ID NO 28900
; LENGTH: 163
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-28900

Query Match 83.3%; Score 15; DB 3; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GGACCTTAGGGCA 16
Db 148 GGACCTAGGGCA 162

RESULT 10
US-09-157-910-6
; Sequence 910, Application US/09157910A
; Patent No. 619744
; GENERAL INFORMATION:

```

APPLICANT: Berleth, Erica
 APPLICANT: Enrike, M. Jane
 APPLICANT: Nadadur, Srikanth
 APPLICANT: Gurcoo, Hir
 APPLICANT: Hein, Alicia
 APPLICANT: Minich, Enrico
 TITLE OF INVENTION: Tumor Necrosis Factor Inhibitory Protein TIP-B1 and Method
 TITLE OF INVENTION: Of Using Same
 FILE REFERENCE: RPP-151-US
 CURRENT APPLICATION NUMBER: US/09/157,910A
 CURRENT FILING DATE: 1998-09-21
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Microsoft Word 97 / MS-DOS Ver. 7.10
 SEQ ID NO: 6
 LENGTH: 783
 TYPE: DNA
 ORGANISM: HOMO SAPIENS
 FEATURE:
 OTHER INFORMATION: This sequence encodes the TIP-B1 peptides of SEQ. ID. #3,
 OTHER INFORMATION: SEQ. ID. #4 and SEQ. ID. #5
 US-09-157-910-6

Query Match
 Best Local Similarity 83.3%; Score 15; DB 3; Length 783;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GGACCTAGGGCAA 16
 Db 730 GGACCTAGGGCAA 744

RESULT 11
 US-09-084-970B-159
 ; Sequence 159, Application US/09484970B
 ; Patent No. 6426186
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Karen A.
 ; APPLICANT: Volkmarth, Wayne
 ; APPLICANT: Walker, Michael G.
 ; TITLE OF INVENTION: BONE REMODELING GENES
 ; FILE REFERENCE: PB-0014 US
 ; CURRENT APPLICATION NUMBER: US/09/484,970B
 ; CURRENT FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 172
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 159
 ; LENGTH: 868
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6426186 234571.8
 ; NAME/KEY: unsure
 ; LOCATION: 23, 27
 ; OTHER INFORMATION: a, t, c, g, or other
 ; US-09-084-970B-159

Query Match
 Best Local Similarity 83.3%; Score 15; DB 3; Length 868;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GGACCTAGGGCAA 16
 Db 820 GGACCTAGGGCAA 834

RESULT 12
 US-09-023-655-508 Application US/09023655
 ; Sequence 508, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Stuart, Susan G.

RESULT 13
 US-09-016-23074/C
 ; Sequence 23074, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED THEREOF
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL011307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 23074
 ; LENGTH: 601
 ; TYPE: DNA

APPLICANT: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 TITLE OF INVENTION: EXPRESSION
 NUMBER OF SEQUENCES: 1508
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeiler, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0355
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 508:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2399 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: NPHGN0T02
 CLONE: 201392
 US-09-023-655-508

Query Match
 Best Local Similarity 83.3%; Score 15; DB 3; Length 2399;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GGACCTAGGGCAA 16
 Db 2294 GGACCTAGGGCAA 2308

; ORGANISM: Human
; US-09-949-016-23074

; Query Match 82.2%; Score 14.8; DB 3; Length 601;
; Best Local Similarity 88.9%; Pred. No. 2.2e+02;
; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Qy 1 CGGACCTAGGGCAAG 18
; Db 190 CAGACCTAGGGCAAG 173

; RESULT 14
; US-09-949-016-169781/C
; Sequence 169781, Application US/09949016

; ; PATENT NO. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 169781
; LENGTH: 601

; SOFTWARE: FastSEQ for Windows Version 4.0
; ;
; ORGANISM: Human
; US-09-949-016-169781

; Query Match 82.2%; Score 14.8; DB 3; Length 601;
; Best Local Similarity 88.9%; Pred. No. 2.2e+02;
; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Qy 1 CGGACCTAGGGCAAG 18
; Db 190 CAGACCTAGGGCAAG 173

; RESULT 15
; US-08-571-758-7
; Sequence 7, Application US/08909984A
; Patent No. 5747275
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerry M.
; APPLICANT: Therrien, Marc
; APPLICANT: Chang, Henry C.
; APPLICANT: Karim, Felix D.
; APPLICANT: Wasserman, David A.

; TITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatternIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,984A
; FILING DATE:
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36 627
; REFERENCE/DOCKET NUMBER: B96-010
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2846 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Pattern Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/571,758

; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B96-010
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ZIP: 94104

; Query Match 82.2%; Score 14.8; DB 2; Length 2846;
; Best Local Similarity 88.9%; Pred. No. 2.5e+02;
; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; Qy 1 CGGACCTAGGGCAAG 18
; Db 214 CGGACCTAGGGCAAG 231

; RESULT 16
; US-08-909-984A-7
; Sequence 7, Application US/08909984A
; Patent No. 5747275
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerry M.
; APPLICANT: Therrien, Marc
; APPLICANT: Chang, Henry C.
; APPLICANT: Karim, Felix D.
; APPLICANT: Wasserman, David A.

; TITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatternIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,984A
; FILING DATE:
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36 627
; REFERENCE/DOCKET NUMBER: B96-010
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ZIP: 94104

; Query Match 82.2%; Score 14.8; DB 2; Length 2846;

Best Local Similarity 88.9%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Length 2846;

Query Match 82.2%; Score 14.8; DB 2; Length 3511;
 Sequence 23, Application US/09560385A
 Best Local Similarity 88.9%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Length 3511;

Qy 1 CGGACCTCTAGGCAAG 18
 Db 214 CGGACCTCTAGGCAAG 231

RESULT 17
 US-08-909-983-7
 Sequence 7, Application US/08909983
 ; GENERAL INFORMATION:
 APPLICANT: Rubin, Gerry M.
 APPLICANT: Therrien, Marc
 APPLICANT: Chang, Henry C.
 APPLICANT: Karim, Felix D.
 APPLICANT: Waserman, David A.
 TITLE OF INVENTION: A Novel Protein Kinase Required for Ras
 TITLE OF INVENTION: Signal Transduction
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/909,983
 FILING DATE: 12-JUN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/571,758
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: B66-010
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-3341
 TELEX: (415) 343-3342
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2846 base pairs
 TYPE: nucleic acid
 STRANDBENESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ; US-08-909-983-7

RESULT 18
 US-01-560-385A-23
 Sequence 23, Application US/09560385A
 ; General Information:
 ; Patent No. 6703363
 ; General Information:
 APPLICANT: Boudand, Ariel
 TITLE OF INVENTION: Recombinant Laminin 5
 FILE REFERENCE: 99-274-C
 CURRENT APPLICATION NUMBER: US/09/560,385A
 CURRENT FILING DATE: 2000-04-28
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 21
 LENGTH: 3585
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(3465)

US-09-560-385A-23
 Sequence 19, Application US/09560385A
 ; General Information:
 ; Patent No. 673363
 ; General Information:
 APPLICANT: Boudand, Ariel
 TITLE OF INVENTION: Recombinant Laminin 5
 FILE REFERENCE: 99-274-C
 CURRENT APPLICATION NUMBER: US/09/560,385A
 CURRENT FILING DATE: 2000-04-28
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 19
 LENGTH: 3511
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (7)..(3507)
 NAME/KEY: misc_feature
 LOCATION: (13)..(36)
 ; US-09-560-385A-19

Query Match 82.2%; Score 14.8; DB 3; Length 3511;
 Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Length 3511;

Qy 1 CGGACCTCTAGGCAAG 18
 Db 1858 CGGACCTCTAGGCAAG 1875

RESULT 19
 US-09-560-385A-21
 Sequence 21, Application US/09560385A
 ; General Information:
 ; Patent No. 6703363
 ; General Information:
 APPLICANT: Boudand, Ariel
 TITLE OF INVENTION: Recombinant Laminin 5
 FILE REFERENCE: 99-274-C
 CURRENT APPLICATION NUMBER: US/09/560,385A
 CURRENT FILING DATE: 2000-04-28
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 21
 LENGTH: 3585
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (60)..(3581)

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; NAME/KEY: sig_peptide
; LOCATION: (60)..(116)
US-09-560-385A-21

Query Match          82.2%; Score 14.8; DB 3; Length 3585;
Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY      1 CGGACCTAGGGCAAG 18
Db      1932 CGGATCCTAGATGCAAG 1949

RESULT 21
US-09-560-385A-17
; Sequence 17, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (60)..(3617)
; NAME/KEY: sig_peptide
; LOCATION: (60)..(110)
; NAME/KEY: misc feature
; LOCATION: (121)..(146)
; US-09-560-385A-17

Query Match          82.2%; Score 14.8; DB 3; Length 3621;
Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY      1 CGGACCTAGGGCAAG 18
Db      1968 CGGATCCTAGATGCAAG 1985

RESULT 22
US-09-560-385A-15
; Sequence 15, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 3759
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3459)
; US-09-560-385A-15

Query Match          82.2%; Score 14.8; DB 3; Length 3759;
Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY      1 CGGACCTAGGGCAAG 18
Db      1810 CGGATCTAGATGCAAG 1827

RESULT 23
US-09-560-385A-13
; Sequence 13, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 3930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(3630)
; NAME/KEY: sig_peptide
; LOCATION: (121)..(171)
; US-09-560-385A-13

Query Match          82.2%; Score 14.8; DB 3; Length 3930;
Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY      1 CGGACCTAGGGCAAG 18
Db      1981 CGGATCCTAGATGCAAG 1998

RESULT 24
US-08-144-121-1
; Sequence 1, Application US/08144121
; Patent No. 5610031
; GENERAL INFORMATION:
; APPLICANT: Burgess, Robert E.
; TITLE OF INVENTION: BIK CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAMIVIE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myer, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE DOCKET NUMBER: (MCH-0780.0) MGP-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-4000
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Single

```

MOLECULE TYPE: cDNA
 TOPOGY: linear
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: 122..3617
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 173..3617

 RESULT 25
 US-08-144-121-1
 Query Match 82.2%; Score 14.8; DB 2; Length 3931;
 Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2;
 Qy 1 CGGACCTAGAGGCAAG 18
 Db 1976 CGGATCTAGATGCAAG 1993

 Sequence 1, Application US/08735893
 Patent No. 5914317
 GENERAL INFORMATION:
 APPLICANT: Burgesson, Robert E.
 ADDRESS: 60 State Street, suite 510
 CITY: BOSTON
 STATE: Massachusetts
 COUNTRY: United States
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/735,893
 FILING DATE: 18-OCT-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/144,121
 FILING DATE: 27-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Paul L.
 REGISTRATION NUMBER: 35,965
 REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: -(617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 1:
 SEQUNENCE CHARACTERISTICS:
 LENGTH: 3931 base pairs
 TYPE: nucleic acid
 STRANEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 122..3617
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 173..3617

 Query Match 82.2%; Score 14.8; DB 3; Length 3971;
 Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2;
 Qy 1 CGGACCTAGAGGCAAG 18
 Db 1976 CGGATCTAGATGCAAG 1993

 RESULT 26
 US-10-841-139-1
 Sequence 1, Application US/10841139
 Patent No. 691631
 GENERAL INFORMATION:
 APPLICANT: Burgesson, Robert E.
 ADDRESS: 60 State Street, suite 510
 CITY: BOSTON
 STATE: Massachusetts
 COUNTRY: United States
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/161,872
 FILING DATE: 1996-09-28
 PRIORITY NUMBER: US 08/735,893
 PRIORITY FILING DATE: 1996-10-23
 NUMBER OF SEQ ID NOS: 14
 PRIORITY FILING DATE: 2003-05-22
 PRIORITY APPLICATION NUMBER: US/09/161,872
 PRIORITY FILING DATE: 1996-09-28
 PRIORITY APPLICATION NUMBER: US 08/735,893
 PRIORITY FILING DATE: 1996-10-23
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 3931
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (122)..(3616)
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (173)..(3616)

 US-10-841-139-1
 Query Match 82.2%; Score 14.8; DB 3; Length 3931;
 Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2;
 Qy 1 CGGACCTAGAGGCAAG 18
 Db 1976 CGGATCTAGATGCAAG 1993

 RESULT 27
 US-09-876-176-1
 Sequence 1, Application US/09876176
 Patent No. 658644
 GENERAL INFORMATION:
 APPLICANT: Reinhard, Christoph
 APPLICANT: Jefferson, Anne B.
 APPLICANT: Den-Otter, Douglas R.
 APPLICANT: Winter, Jill A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 TITLE OF INVENTION: NEOPLASTIC DISEASE USING INHIBITORS OF LAMININ5BETA3
 FILE REFERENCE: PP-01702_002/200130-523
 CURRENT APPLICATION NUMBER: US/09/876,176
 CURRENT FILING DATE: 2001-06-06
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 3971
 TYPE: DNA
 ORGANISM: Homo sapiens
 US 09-876-176-1

 Query Match 82.2%; Score 14.8; DB 3; Length 3971;
 Best Local Similarity 88.9%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2;
 Qy 1 CGGACCTAGAGGCAAG 18

Db 1948 ||||| CGGATCCTAGTGCAG 1965

RESULT 28
US 09-919-172-15
Sequence 15, Application US/09919172
Patent No. 6673545
GENERAL INFORMATION:
APPLICANT: Paris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL program
SEQ ID NO 15
LENGTH: 4108
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673545 3615080CB1

US-09-919-172-15

Query Match 82.2%; Score 14.8; DB 3; Length 4108;
Best Local Similarity 88.9%; Pred. No. 2.66+02; Mismatches 16; Conservative 0; Indels 0; Gaps 0;

Qy 1 CGGACCTCTAGGGCAAG 18
||| ||||| ||||| 2082

Db 2065 CGGATCTCTAGATGCCAG 2082

RESULT 29
US-07-841-646-3
Sequence 3, Application US/07841646
Patent No. 5266583
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,998
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: FITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001LCF6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: NUCLEAR ACID
STRANDBEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1
FEATURE:
NAME/KEY: misc feature
LOCATION: 10413..10414
OTHER INFORMATION: /label= GAP-1
OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 10596..10891
OTHER INFORMATION: /label= EXON-2
FEATURE:
NAME/KEY: misc feature
LOCATION: 10660..10961
OTHER INFORMATION: /label= GAP-2

OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO BE MISSING BETWEEN POSITION 10960 AND 10961 IN THIS SEQUENCE."

FEATURE: NAME/KEY: exon
LOCATION: 11059..11211
OTHER INFORMATION: /label= EXON-3

FEATURE: NAME/KEY: misc feature
LOCATION: 11351..11352
OTHER INFORMATION: /label= GAP-3
OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO BE MISSING BETWEEN POSITIONS 11351 AND 11352 IN THIS SEQUENCE."

FEATURE: NAME/KEY: exon
LOCATION: 11420..11617
OTHER INFORMATION: /label= EXON-4

FEATURE: NAME/KEY: misc feature
LOCATION: 11721..11722
OTHER INFORMATION: /label= GAP-4
OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO BE MISSING BETWEEN POSITIONS 11721 AND 11722 IN THIS SEQUENCE."

FEATURE: NAME/KEY: exon
LOCATION: 13354..13436
OTHER INFORMATION: /label= EXON-5

FEATURE: NAME/KEY: exon
LOCATION: 15044..15160
OTHER INFORMATION: /label= EXON-6

FEATURE: NAME/KEY: exon
LOCATION: 17245..17410
OTHER INFORMATION: /label= EXON-7

US-07-841-646-3

Query Match Best Local Similarity 82.2%; Score 14.8; DB 2; Length 17410;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	CCGACCCCTAGGCCAAG	18
Db	14427	CAGACCCTAGGCCAAGG	14444

RESULT 30

US-08-147-023-3

; Sequence 3, Application US/08147023

; Patent No. 5468845

; GENERAL INFORMATION:

; APPLICANT: OPPERMAN, HERMANN

; APPLICANT: OZKAYNAK, ENGIN

; APPLICANT: KUBERSAMPATH, THANGAVEL

; APPLICANT: RUGER, DAVID C.

; APPLICANT: PANG, ROY H. L.

TITLE OF INVENTION: OSTEOGENIC DEVICES

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: 53 STATE STREET

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,023

FILING DATE: 21-FEB-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 810,560

FILING DATE: 20-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 827,052

FILING DATE: 28-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 660,162

FILING DATE: 22-FEB-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 621,988

FILING DATE: 04-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 621,849

FILING DATE: 04-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 616,374

FILING DATE: 21-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 600,024

FILING DATE: 18-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 599,543

FILING DATE: 18-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 579,865

FILING DATE: 07-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 569,920

FILING DATE: 20-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 483,913

FILING DATE: 22-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 422,613

FILING DATE: 17-OCT-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 315,342

FILING DATE: 23-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 232,630

FILING DATE: 15-AUG-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 179,460

FILING DATE: 08-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: FITCHER, EDMUND R.

REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: CRP-001CP6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/248-7100

TELEFAX: 617/248-7100

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 17410 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE: homosapiens

ORGANISM: homo sapiens

FEATURE:

NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1

FEATURE: NAME/KEY: misc feature
LOCATION: 10413..10414
OTHER INFORMATION: /label= GAP-1

OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN THIS SEQUENCE."

FEATURE:

NAME/KEY: exon

LOCATION: 10696..10891

OTHER INFORMATION: /label= EXON-2

FEATURE:

NAME/KEY: misc_feature

LOCATION: 10960..10961

OTHER INFORMATION: /label= GAP-2

OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO BE MISSING BETWEEN POSITION 10960 AND 10961 IN THIS SEQUENCE."

FEATURE:

NAME/KEY: exon

LOCATION: 11059..11211

OTHER INFORMATION: /label= EXON-3

FEATURE:

NAME/KEY: misc_feature

LOCATION: 11351..11352

OTHER INFORMATION: /label= GAP-3

OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO BE MISSING BETWEEN POSITIONS 11351 AND 11352 IN THIS SEQUENCE."

FEATURE:

NAME/KEY: exon

LOCATION: 11420..11617

OTHER INFORMATION: /label= EXON-4

FEATURE:

NAME/KEY: misc_feature

LOCATION: 11721..11722

OTHER INFORMATION: /label= GAP-4

OTHER INFORMATION: /note= "APPROXIMATELY BASES ARE ESTIMATED TO BE MISSING BETWEEN POSITIONS 11721 AND 11722 IN THIS SEQUENCE."

FEATURE:

NAME/KEY: exon

LOCATION: 13354..13436

OTHER INFORMATION: /label= EXON-5

FEATURE:

NAME/KEY: exon

LOCATION: 15044..15160

OTHER INFORMATION: /label= EXON-6

FEATURE:

NAME/KEY: exon

LOCATION: 17245..17410

OTHER INFORMATION: /label= EXON-7

US-08-147-023-3

Query Match 92.2%; Score 14.8; DB 2; Length 17410;
 Best Local Similarity 88.9%; Pred. No. 3e+02; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	CGGACCCCTAGAGGCGAAG	18
Db	14427	CAGACCTAGAGGCGAAG	14444

Search completed: April 15, 2006, 20:30:30
 Job time : 205 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om nucleic - nucleic search, using bw model

Run on: April 15, 2006, 19:30:59 ; Search time 673 Seconds
 (without alignments)

17.8.253 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18

Sequence: 1 cggacccttaggcaag 18

Scoring table: IDENTITY_NUC

Gapov 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 300 summaries

Database : N_Geneseq_21:*

1: geneseqn1980s:.*

2: geneseqn1990s:.*

3: geneseqn2000s:.*

4: geneseqn2001as:.*

5: geneseqn2001bs:.*

6: geneseqn2002as:.*

7: geneseqn2002bs:.*

8: geneseqn2003as:.*

9: geneseqn2003bs:.*

10: geneseqn2003cs:.*

11: geneseqn2003ds:.*

12: geneseqn2004as:.*

13: geneseqn2004bs:.*

14: geneseqn2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	18	100.0	18 12 ADG75398	Adg75398 Human kin
2	18	100.0	18 12 ADG75391	Adg75391 Human kin
3	18	100.0	18 14 AEA46548	Aea46548 Kinase su
4	18	100.0	18 14 AEA46538	Aea46538 Kinase su
5	18	100.0	18 14 AEA46561	Aea46561 Kinase su
6	18	100.0	120 14 AEA46534	Aea46534 Kinase su
7	18	100.0	121 14 AEA46558	Aea46558 Kinase su
8	18	100.0	2501 14 AEA46557	Aea46557 Human kin
9	18	100.0	4034 14 AEA46544	Aea46544 Mouse kin
10	18	100.0	4094 12 AAT72155	Aat72155 Mouse kin
11	18	100.0	4094 12 AAT72394	Aat72394 Mouse kin
12	16	88.9	16 14 AEA46541	Aea46541 Kinase su
13	16	88.9	376 6 ABL67488	Abi67488 Thyroid c
14	15.4	85.6	376 6 ABL69201	Abi69201 Prostate
15	15.4	85.6	388 10 ADP80786	Adp80786 Leukaemia
16	15.4	85.6	514 4 AAK88398	Aak88398 Human dig
17	15.4	85.6	514 5 AAS39499	Aas39499 CDNA enco
18	15.4	85.6	514 9 ADB32225	Adb32225 Human nov
19	15.4	85.6	986 10 ADP82177	Adp82177 Leukaemia

c 20 15.4 85.6 1797 12 ADG24821 Human sof
 c 21 15.4 85.6 9645 12 ADQ18079 Human sof
 c 22 15.4 85.6 2001 14 ADZ59509 Secondary
 c 23 15.4 85.6 22475 12 ADQ97938 Human can
 c 24 15.4 85.6 191150 12 ADM69029 Human pla
 c 25 15 83.3 230 12 ADG040825 Human leu
 c 26 15 83.3 50 12 ADP10220 50-mer ol
 c 27 15 83.3 51 4 AAT76987 Human sil
 c 28 15 83.3 51 4 AAT76986 Human sil
 c 29 15 83.3 75 6 ABR95689 Tumour su
 c 30 15 83.3 163 3 AAC24825 Human sec
 c 31 15 83.3 230 12 ADG040825 Human ctn
 c 32 15 83.3 45 6 ABU38407 Human col
 c 33 15 83.3 412 9 ACT49943 Human leu
 c 34 15 83.3 444 6 ABK36157 DNA sequ
 c 35 15 83.3 61 13 ACF83765 Human car
 c 36 15 83.3 478 9 ACT29337 Human adu
 c 37 15 83.3 495 12 ADD00107 Novel hum
 c 38 15 83.3 495 12 ADN98538 Novel hum
 c 39 15 83.3 554 4 AAS35449 Human car
 c 40 15 83.3 554 10 ADB45528 Human car
 c 41 15 83.3 554 13 ADD65946 Human car
 c 42 15 83.3 627 10 ADB47513 Human cdv
 c 43 15 83.3 645 9 AAD57225 Human Cdp
 c 44 15 83.3 764 12 ADP10522 Reference
 c 45 15 83.3 825 3 AAAX59670 DNA encod
 c 46 15 83.3 868 6 ABK36158 cDNA seq
 c 47 15 83.3 779 11 ABM01377 Human cdp
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 c 49 15 83.3 784 6 ABG9835 Human cdv
 c 50 15 83.3 803 14 AER1946 Novel hum
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 c 52 15 83.3 868 6 ABR70502 Human bon
 c 53 15 83.3 2278 11 ABM01377 Human cdp
 c 54 15 83.3 2399 11 ADI31182 Human
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 c 56 15 83.3 5760 4 ABU3249 Novel hum
 c 57 15 83.3 833 11 ADB32627_2 Human cdp
 c 58 15 83.3 110000 13 ABK3516 Human can
 c 59 15 83.3 123937 13 ADB33516 Human can
 c 60 14.8 82.2 399 3 AAB82091 Human can
 c 61 14.8 82.2 1115 13 ADX6403 Plant ful
 c 62 14.8 82.2 1149 11 ACT13134 Banana ge
 c 63 14.8 82.2 1149 11 ACT13134 Banana ge
 c 64 14.8 82.2 2044 6 ADR62571 Cotton cd
 c 65 14.8 82.2 2044 3 ABK35181 Human cdp
 c 66 14.8 82.2 2204 3 AAB53270 Human can
 c 67 14.8 82.2 2605 8 ACC7209 Human pho
 c 68 14.8 82.2 2661 9 ADL1557 Human kin
 c 69 14.8 82.2 2703 9 ADL1557 Human kin
 c 70 14.8 82.2 2846 2 AAT72156 Human ksr
 c 71 14.8 82.2 2870 4 ABU15818 Drosophil
 c 72 14.8 82.2 3006 4 ABU16372 Drosophil
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 c 74 14.8 82.2 3342 13 ADR08122 Full leng
 c 75 14.8 82.2 3357 12 ADQ64764 Novel hum
 c 76 14.8 82.2 3469 3 AAC83728 Human lam
 c 77 14.8 82.2 3511 2 AAC83726 Human lam
 c 78 14.8 82.2 3516 2 AAV29044 Open read
 c 79 14.8 82.2 3519 14 ADV67470 Nucleotid
 c 80 14.8 82.2 3585 3 AAC83727 Human lam
 c 81 14.8 82.2 3621 3 AAC83725 Human lam
 c 82 14.8 82.2 3759 3 AAC83724 Human lam
 c 83 14.8 82.2 3810 2 AAC83726 Human nov
 c 84 14.8 82.2 3930 2 AAQ89871 Laminin B
 c 85 14.8 82.2 3930 2 AAC83723 Human lam
 c 86 14.8 82.2 3971 6 AAD28066 LamininB
 c 87 14.8 82.2 3971 8 ABX76133 Lung canc
 c 88 14.8 82.2 3971 8 ABX76390 Lung canc
 c 89 14.8 82.2 3971 8 ACC72087 Human NOV
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 c 91 14.8 82.2 3971 10 ADC39001 Cancer/lan
 c 92 14.8 82.2 3971 13 ACN37576 Tumour-ab

93	14.8	82.2	4108	6	AB52737	c	166	14.4	80.0	103747	6	AB088139
94	14.8	82.2	4108	8	ABX77550	c	167	14.4	80.0	110000	12	ADN4685-17
95	14.8	82.2	4108	8	ABX5559	c	168	14.4	80.0	110000	12	ADN47551-03
96	14.8	82.2	4108	14	ADV5764	c	169	14.4	80.0	110000	12	ADN46123-17
97	14.8	82.2	4667	2	AVV2043	c	170	14.4	80.0	110000	12	ADN47209-03
98	14.8	82.2	4816	10	ADE4538	c	171	14.4	80.0	110000	12	ADN46494-17
99	14.8	82.2	4815	10	ADE4542	c	172	14.4	80.0	110000	14	AEB4901_21
100	14.8	82.2	5913	12	ADJ6596	c	173	14.4	80.0	110000	14	ACM4845
101	14.8	82.2	17350	2	AAQ72108	c	174	14.4	80.0	115218	8	ACM48485
102	14.8	82.2	17410	12	AEO5142	c	175	14.4	80.0	116704	11	ACN44818
103	14.8	82.2	17410	2	AAT18381	c	176	14.4	80.0	127767	13	ARD33584
104	14.8	82.2	17410	2	AAV15205	c	177	14.4	80.0	127767	13	AUR67023
105	14.8	82.2	17410	2	AAX0230	c	178	14.4	80.0	127767	14	AAB090769
106	14.8	82.2	17410	2	AAZ27575	c	179	14.4	80.0	134499	3	AAP22285
107	14.8	82.2	17410	10	ADU2678	c	180	14.4	80.0	142976	13	ARD32612
108	14.8	82.2	17410	12	ADE72749	c	181	14.4	80.0	150201	12	ADU213203
109	14.8	82.2	17410	12	ADM80487	c	182	14.4	80.0	329019	13	ARD32707
110	14.8	82.2	17410	13	ADD03609	c	183	14.4	77.8	247	2	AAR14378
111	14.8	82.2	17415	2	AAT16139	c	184	14.4	77.8	315	2	AAB09484
112	14.8	82.2	17415	2	AAV80733	c	185	14.4	80.0	134499	3	AAP22285
113	14.8	82.2	17415	3	AAAS5897	c	186	14.4	80.0	142976	13	ARD32612
114	14.8	82.2	97700	10	ADL13678	c	187	14.4	77.8	585	12	AUP57048
115	14.8	82.2	101786	3	AAF22293	c	188	14.4	77.8	616	3	AAP07978
116	14.8	82.2	110000	12	ABD07173_3	c	189	14.4	77.8	616	13	AUDS3819
117	14.8	82.2	117750	13	AAC52653	c	190	14.4	77.8	616	14	ABG90769
118	14.8	80.0	201	13	ADG0630	c	191	14.4	77.8	585	6	ABP62977
119	14.4	80.0	364	3	AAC22364	c	192	14.4	77.8	585	10	ADU57048
120	14.4	80.0	483	3	ABZ5573	c	193	14.4	77.8	585	12	AUP72219
121	14.4	80.0	380	13	ADR1486	c	194	14	77.8	6274	10	ADU09798
122	14.4	80.0	419	8	ABX45259	c	195	14	77.8	8919	4	AAB13054
123	14.4	80.0	475	10	ADB23091	c	196	14	77.8	8919	8	AAB22305
124	14.4	80.0	475	10	ADB23091	c	197	14	77.8	11000	6	ABP55320_0
125	14.4	80.0	479	6	ABL64293	c	198	14	77.8	11000	6	ABP55320_0
126	14.4	80.0	483	3	AAC8139	c	199	14	77.8	2445	12	AUQ63262
127	14.4	80.0	498	4	AKR7223	c	200	14	77.8	11000	14	ADU53957
128	14.4	80.0	552	6	ABK9877	c	201	14	77.8	189013	8	AIR6741
129	14.4	80.0	564	8	ABZ77962	c	202	14	77.8	189013	10	ADB20856
130	14.4	80.0	581	8	ACD20381	c	203	14	77.8	189013	10	ADB87945
131	14.4	80.0	592	12	ACHT3816	c	204	14	77.8	189013	10	ADU96928
132	14.4	80.0	621	4	ABL2863	c	205	14	77.8	189013	10	ADU92119
133	14.4	80.0	636	5	ABV5466	c	206	14	77.8	189013	10	ADU92119
134	14.4	80.0	658	3	AAC57768	c	207	14	77.8	189013	13	ADU92119
135	14.4	80.0	659	8	ABD25299	c	208	14	77.8	189013	13	ADU92119
136	14.4	80.0	939	3	AAC57769	c	209	14	77.8	189013	10	ADU92119
137	14.4	80.0	1022	2	AZZ11769	c	210	14	77.8	189013	10	ADU92119
138	14.4	80.0	2136	13	ADX4721	c	211	14	77.8	189013	10	ADU92119
139	14.4	80.0	2195	12	ADM6717	c	212	14	77.8	189013	13	ADU92119
140	14.4	80.0	2621	4	ABL28662	c	213	14	77.8	189013	13	ADU92119
141	14.4	80.0	2754	3	AAC5843	c	214	14	77.8	189013	13	ADU92119
142	14.4	80.0	2754	6	ABZ12391	c	215	14	77.8	189013	13	ADU92119
143	14.4	80.0	2754	8	ADU8022	c	216	14	77.8	189013	13	ADU92119
144	14.4	80.0	2754	12	ADU72372	c	217	14	77.8	189013	13	ADU92119
145	14.4	80.0	3153	10	ADU2173	c	218	14	77.8	189013	13	ADU92119
146	14.4	80.0	4857	4	AAK80786	c	219	14	76.7	209083	20	ACT02856
147	14.4	80.0	5122	4	AAK80784	c	220	14	76.7	209083	20	ADU5003
148	14.4	80.0	5122	4	AAK80787	c	221	14	76.7	209083	20	ADU5003
149	14.4	80.0	5122	4	AAK80785	c	222	14	76.7	209083	20	ADU5003
150	14.4	80.0	6951	6	ADG2852	c	223	14	76.7	209083	20	ADU5003
151	14.4	80.0	6955	10	ADU9926	c	224	14	76.7	209083	20	ADU5003
152	14.4	80.0	7036	8	ABZ257963	c	225	14	76.7	209083	20	ADU5003
153	14.4	80.0	7376	4	AAK63043	c	226	14	76.7	209083	20	ADU5003
154	14.4	80.0	7888	13	ADU3507	c	227	14	76.7	209083	20	ADU5003
155	14.4	80.0	8323	2	AAQ58700	c	228	14	76.7	209083	20	ADU5003
156	14.4	80.0	8323	2	AAQ5842	c	229	14	76.7	209083	20	ADU5003
157	14.4	80.0	8323	2	AAU0508	c	230	14	76.7	209083	20	ADU5003
158	14.4	80.0	8323	10	ADU9926	c	231	14	76.7	209083	20	ADU5003
159	14.4	80.0	10367	2	AAQ58701	c	232	14	76.7	209083	20	ADU5003
160	14.4	80.0	10357	2	AAU05057	c	233	14	76.7	209083	20	ADU5003
161	14.4	80.0	10367	2	AAU07067	c	234	14	76.7	209083	20	ADU5003
162	14.4	80.0	18443	2	AAV8342	c	235	14	76.7	209083	20	ADU5003
163	14.4	80.0	19986	13	ADU56481	c	236	14	76.7	209083	20	ADU5003
164	14.4	80.0	21429	4	AAU57362	c	237	14	76.7	209083	20	ADU5003
165	14.4	80.0	71953	11	ACN44552	c	238	14	76.7	209083	20	ADU5003

Abq88139 Human ost

Continuation (18 o

Continuation (4 of

Continuation (

C	239	13.8	76.7	353	4	ABA55727		DT	11-MAR-2004	(first entry)
C	240	13.8	76.7	353	4	AAI5382	Aai5382 Probe #40	XX		
C	241	13.8	76.7	353	4	ABA45235	Human kinase suppressor of Ras (KSR)-specific oligonucleotide.	DE		
C	242	13.8	76.7	353	4	ABA54510	Abs45235 Human bra	XX		
C	243	13.8	76.7	353	4	AAK9426	Aak2426 Human bra	KW		
C	244	13.8	76.7	353	4	AKR01949	Aak33949 Human bra	KW		
C	245	13.8	76.7	353	4	ABA29053	Abs29053 Human liv	KW		
C	246	13.8	76.7	353	5	AAI03861	Aai03861 Probe #38	KW		
C	247	13.8	76.7	353	6	AB503981	Abs03981 Human gen	KW		
C	248	13.8	76.7	357	11	ACU33699	Acu133699 Rice abio	KW		
C	249	13.8	76.7	369	6	ABK72169	Abi72169 Lymphoma	KW		
C	250	13.8	76.7	369	12	ADM79223	Adm79223 Mouse 1ym	KW		
C	251	13.8	76.7	371	4	ABA75195	Abi75195 Human foe	OS		
C	252	13.8	76.7	371	4	AAI55744	Aai55744 Probe #24	XX		
C	253	13.8	76.7	371	4	AAK9827	Aak9827 Human bra	XX		
C	254	13.8	76.7	371	4	AKC23730	Aak23730 Human bra	KW		
C	255	13.8	76.7	371	6	AB823331	Abs23331 Human gen	KW		
C	256	13.8	76.7	374	4	ABA73972	Abi73972 Human foe	KW		
C	257	13.8	76.7	374	4	AAI4421	Aai4421 Probe #23	KW		
C	258	13.8	76.7	374	4	AAK8592	Aak8592 Human bra	PR		
C	259	13.8	76.7	374	4	AKC2425	Aak2425 Human bra	PR	30-MAY-2002; 2002US-0384228P.	
C	260	13.8	76.7	374	4	ABA82277	Abs82277 Human liv	XX	03-APR-2003; 2003US-0460023P.	
C	261	13.8	76.7	374	6	AB522353	Abs22353 Human gen	PA		
C	262	13.8	76.7	375	6	ABA76814	Abi76814 Human ORF	XX		
C	263	13.8	76.7	378	4	AAI23005	Aai23005 Probe #12	XX		
C	264	13.8	76.7	378	4	ABA68096	Aba68096 Human feo	DR		
C	265	13.8	76.7	378	4	AAI48305	Aai48305 Probe #16	XX		
C	266	13.8	76.7	378	4	ABA0162	Aba0162 Human bra	PT		
C	267	13.8	76.7	378	4	ABA35125	Aba35125 Probe #13	PT		
C	268	13.8	76.7	378	4	AKR2235	Akr2235 Human bra	PT		
C	269	13.8	76.7	378	4	AAK16483	Aak16483 Human bra	PT		
C	270	13.8	76.7	378	4	ABA51841	Aba51841 Human liv	PT		
C	271	13.8	76.7	378	5	AAI08668	Aai08668 Probe #6	XX		
C	272	13.8	76.7	378	6	ABA516285	Aba516285 Human gen	PS		
C	273	13.8	76.7	383	4	AAI23099	Aai23099 Probe #13	XX		
C	274	13.8	76.7	383	4	AAI21743	Aai21743 Probe #11	CC		
C	275	13.8	76.7	383	4	AAI21300	Aai21300 Probe #11	CC		
C	276	13.8	76.7	383	4	ABA68190	Aba68190 Human feo	CC		
C	277	13.8	76.7	383	4	ABA66383	Aba66383 Human feo	CC		
C	278	13.8	76.7	383	4	ABA66819	Aba66819 Human feo	CC		
C	279	13.8	76.7	383	4	AAI47027	Aai47027 Probe #15	CC		
C	280	13.8	76.7	383	4	AAI46576	Aai46576 Probe #15	CC		
C	281	13.8	76.7	383	4	AAI48401	Aai48401 Probe #15	CC		
C	282	13.8	76.7	383	4	ABA48900	Aba48900 Human bre	CC		
C	283	13.8	76.7	383	4	ABA48478	Aba48478 Human bra	CC		
C	284	13.8	76.7	383	4	ABA50244	Aba50244 Human bre	CC		
C	285	13.8	76.7	383	4	ABA35198	Aba35198 Probe #13	CC		
C	286	13.8	76.7	383	4	ABA33444	Aba33444 Probe #11	CC		
C	287	13.8	76.7	383	4	ABA33802	Aba33802 Probe #11	CC		
C	288	13.8	76.7	383	4	AAK42320	Aak42320 Human bra	CC		
C	289	13.8	76.7	383	4	AAK40539	Aak40539 Human bra	CC		
C	290	13.8	76.7	383	4	AAK40972	Aak40972 Human bra	CC		
C	291	13.8	76.7	383	4	AAI88464	Aai88464 Human pool	CC		
C	292	13.8	76.7	383	4	AAK15248	Aak15248 Human bra	CC		
C	293	13.8	76.7	383	4	AAK14798	Aak14798 Human bra	CC		
C	294	13.8	76.7	383	4	AAK16565	Aak16565 Human bra	CC		
C	295	13.8	76.7	383	4	ABA50102	Aba50102 Human liv	CC		
C	296	13.8	76.7	383	4	ABA41936	Aba41936 Human liv	CC		
C	297	13.8	76.7	383	4	ABA40556	Aba40556 Human liv	CC		
C	298	13.8	76.7	383	5	ABA07428	Aba07428 Probe #74	DE		
C	299	13.8	76.7	383	5	AAU07004	Aau07004 Probe #69	XX		
C	300	13.8	76.7	383	5	AAT08746	Aat08746 Probe #87	AC		

ALIGNMENTS

RESULT 1 Human kinase suppressor of Ras (KSR) antisense oligonucleotide #3.

RESULT 1

ADG7598

ID ADG75398 standard; DNA; 18 BP.

XX

AC ADG75398;

XX

DE

DE

Query Match Best Local Similarity 100.0%; Score 18; DB 12; Length 18; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

OY 1 CGGACCTCTAGGGCAAG 18

Db 1 COGACCCTAGGCGAAG 18

RESULT 2 ADG75391/c ID ADG75391 standard; DNA; 18 BP.

RESULT 2 ADG75391/c ID ADG75391 standard; DNA; 18 BP.

RESULT 2 ADG75391/c ID ADG75391 standard; DNA; 18 BP.

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RESULT 2 ADG75391/c ID ADG75391 standard; DNA; 18 BP.

XX
OS Homo sapiens.
XX
WO2003101386-A2.
XX
PD 11-DEC-2003.
XX
PP 29-MAY-2003; 2003WO-US016961.
XX
PR 30-MAY-2002; 2002US-0344228P.
XX
PR 03-APR-2003; 2003US-0460023P.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PA Kolesnick RN, Xing HR;
XX
PT WPI; 2004-053335/05.
XX
PS New antisense oligonucleotides complementary to a region of kinase suppressor of Ras (KSR) RNA which inhibit KSR expression, useful for treating or inhibiting progression of cancer, e.g. pancreatic, lung, skin, or bladder cancer.
XX
PS Claim 8; SEQ ID NO 8; 120pp; English.
XX
PT The invention comprises antisense oligonucleotides which are designed to inhibit the expression of the kinase suppressor of Ras (KSR) gene. The antisense oligonucleotides of the invention are useful for treating or inhibiting the progression of cancer, such as: pancreatic cancer, lung cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal cancer, breast cancer, ovarian cancer, stomach cancer, head and neck cancer, oesophageal cancer, prostate cancer, leukaemia, lymphoma, and neuroblastoma. The present DNA sequence represents a human KSR-specific antisense oligonucleotide of the invention.
XX
SQ Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 other;
XX
Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGACCTAGGGCAAG 18
AC |||||
Db 18 CGGACCTAGGGCAAG 1

RESULT 3
AE46548
ID AE46548 standard; DNA; 18 BP.
XX
AC AE46548;
XX
DT 25-AUG-2005 (first entry)
XX
DE Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:15.
XX
KW Kinase suppressor of Ras; KSR; cyostatic; neoplasm; pancreas tumor;
KW liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
KW gastrointestinal disease; respiratory disease; genitourinary disease;
KW endocrine disease; bladder tumor; colon tumor; intestine tumor;
KW head & neck tumor; leukemia; hematological disease; Lymphoma;
KW immune disorder; esophagus tumor; breast tumor; stomach tumor;
KW nervous system tumor; neurological disease; ovary tumor;
KW gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
KW cardiovascular disease; antinease Oligonucleotide; antisense therapy;
KW prostate tumor; andrology; cancer; hyperproliferation.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN WO2005056756-A2.

XX
PD 23-JUN-2005.
XX
PP 03-DEC-2004; 2004WO-US040506.
XX
PR 03-DEC-2003; 2003US-00727358.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PT Kolesnick RN, Xing HR;
XX
DR WPI; 2005-445165/45.
XX
PS Example 2; SEQ ID NO 15; 186pp; English.
XX
PT The invention relates to an oligonucleotide (1) which is substantially complementary to a region of kinase suppressor of Ras (KSR) RNA, where the oligonucleotide inhibits the expression of KSR. Also included are the following: an oligonucleotide (II), which is substantially complementary to a translation initiation site, 5' untranslated region, coding region or 3' untranslated region of mRNA encoding mammalian KSR; an antisense oligonucleotide (III) comprising a sequence substantially complementary to the Cai region of KSR; an antisense oligonucleotide (IV) comprising a sequence substantially complementary to nucleotides 124-243 of the coding sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion; an antisense oligonucleotide (V) comprising a sequence chosen from AE46539, AE46540 and AE46541; and a recombinant DNA molecule (VI) comprising a nucleic acid sequence which encodes on transcription an antisense RNA complementary to mammalian KSR RNA or its portion; a cell (VII) transfected with (VI); an expression vector (VII) capable of expressing a nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide/nucleic acid inhibits the expression of KSR; an expression vector (VZ) capable of expressing an oligonucleotide which is substantially complementary to the Cai region of the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the expression of KSR; a pharmaceutical composition (PC1) comprising (I) and a carrier or diluent; a composition (C2) comprising one or more chemotherapeutic or radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA encoding mammalian KSR and which inhibits KSR expression; a composition (C3) comprising an expression vector and a carrier or diluent, where the expression vector is capable of expressing nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the nucleic acid inhibits the expression of KSR; a composition (M1) comprising a mammalian KSR comprising contacting a cells which express KSR with a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or preventing (M2) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of KSR in a mammal comprising administering to the mammal a compound or agent which inhibits the expression of mammalian KSR protein; treating or preventing (M3) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of KSR in a mammal comprising expressing expressing in the mammal or administering to the mammal therapeutically effective amount of a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or inhibiting (M4) the progression of cancer in a mammal comprising administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting angiogenesis of tumor cells in a mammal; by administering a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting or reducing VEGF expression or activity in a mammal, by administering a compound or agent that inhibits the expression of mammalian KSR protein; stimulating angiogenesis in a mammal comprising administering to a mammal a therapeutically effective amount of a compound or agent which activates the expression of mammalian KSR protein or a vector expressing mammalian KSR, identifying compounds or agents which inhibit the expression of KSR, by incubating a cell expressing KSR in the presence and absence of a

candidate compound or agent, and detecting or measuring the expression of KSR in the presence and absence of a candidate compound or agent, where a decrease in the expression of KSR in the presence of the candidate compound or compound or agent versus in the absence of the candidate compound or agent indicates that the compound or agent inhibits the expression of KSR ; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the expression of mammalian KSR comprising contacting cells which express KSR with (I), where expression of mammalian KSR is inhibited. (II) is useful for conferring radiosensitivity to ionizing radiation in tumor cells in a mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is useful for inhibiting or reducing VEGF expression or activity in a mammal. The methods are useful for treating or preventing hyperproliferative condition associated with expression of gf-Ras or heightened expression of Ras in a mammal and for treating or inhibiting the progression of cancer in a mammal. The cancer is chosen from, pancreatic cancer, lung cancer, skin cancer, urinary tract cancer, bladder cancer, leukemia, liver cancer, thyroid cancer, colon cancer, intestinal cancer, lymphoma, neuroblastoma, head and neck cancer, breast cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate cancer. The present sequence represents a KSR antisense oligonucleotide.

Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
Sequence 19 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; **Score** 18; **DB** 14; **Length** 18;
Best Local Similarity 100.0%; **Pred.** No. 21;
Matches 18; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 CGGACCTAGAGGCCAAG 18
Db 1 CGGACCTAGAGGCCAAG 18

RESULT 4

NEA46538
ID AEA46538 **Standard**; **DNA**; 18 **BP**.
XX
AC AEA46538;
XX
DT 25-AUG-2005 **(first entry)**

XX Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:5.
XX Kinase suppressor of Ras; KSR; cytostatic; neoplasm; pancreas tumor; liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor; gastrointestinal disease; respiratory disease; genitourinary disease; endocrine disease; bladder tumor; colon tumor; intestine tumor; head & neck tumor; leukemia; hematological disease; lymphoma; immune disorder; esophagus tumor; breast tumor; stomach tumor; nervous system tumor; neurological disease; ovary tumor; gynecology and obstetrics; ss; angiogenesis disorder; antisense therapy; cardiovascular disease; anti-sense oligogenetic disorder; antisense therapy; prostate tumor; andrology; cancer; hyperproliferation; Homo sapiens. **OS** Mus sp. **OS** Synthetic. **PN** WO200556756-A2.

XX 03-DEC-2004; 2004WO-US040506.
PR 03-DEC-2003; 2003US-00727358.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Kolenacik RN, Xing HR;
XX DR WPI; 2005-445165/45.

PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression, useful for inhibiting expression of mammalian KSR and treating ovarian cancer.

PT hyperproliferative conditions such as lung cancer, skin cancer, and ovarian cancer.

PT The invention relates to an oligonucleotide (I) which is substantially complementary to a region of kinase suppressor of Ras (KSR) RNA, where the oligonucleotide inhibits the expression of KSR. Also included are the following: an oligonucleotide (II) which is substantially complementary to a translation initiation site, 5' untranslated region, coding region or 3' untranslated region of RNA encoding mammalian KSR; an antisense oligonucleotide (III) comprising a sequence substantially complementary to the 3' region of KSR; an antisense oligonucleotide (IV) comprising a sequence substantially complementary to the 5' region of KSR; an antisense oligonucleotide (V) comprising a sequence substantially complementary to the 5' region of mouse KSR; or nucleotides 97-215 of human KSR or its portion; an antisense oligonucleotide (VI) comprising a sequence chosen from ARA46539, AEA46540 and ARA46541; and ; a recombinant DNA molecule (VII) comprising a nucleic acid sequence which encodes on transcription an antisense RNA complementary to mammalian KSR RNA or its portion; a cell (VII) transfected with (VII); an expression vector (VII) capable of expressing a nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide/nucleic acid inhibits the expression of KSR; an expression vector (VII) capable of expressing an oligonucleotide which is substantially complementary to the 3' region of the coding sequence of KSR RNA, or its portion/fragment, where the expression of KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the expression of KSR; a carrier or diluent; a composition (C1) comprising (I) and a carrier or diluent; a composition (C2) comprising one or more chemotherapeutic or radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA encoding mammalian KSR and which inhibits KSR expression; a composition (C3) comprising an expression vector and a carrier or diluent, where the expression vector is capable of expressing nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the nucleic acid inhibits the expression of KSR; cells which express KSR with a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or preventing (M2) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising administering to the mammal a compound or agent which inhibits the expression of mammalian KSR protein; treating or preventing (M1) the expression of mammalian KSR associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising expressing in the mammal or administering to the mammal therapeutically effective amount of a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or inhibiting (M4) the progression of cancer in a mammal comprising administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting angiogenesis of tumor cells in a mammal, by administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting or reducing VEGF expression or activity in a mammal, by administering a compound or agent that inhibits the expression of mammalian KSR protein; stimulating angiogenesis in a mammal comprising administering to a mammal a therapeutically effective amount of a compound or agent which activates the expression of mammalian KSR protein or a vector expressing mammalian KSR; identifying compounds or agents which inhibit the expression of KSR, by incubating a cell expressing KSR in the presence and absence of a candidate compound or agent, and detecting or measuring the expression of KSR in the presence and absence of a candidate compound or agent, where a decrease in the expression of KSR in the presence of the candidate compound or agent versus in the absence of the candidate compound or agent indicates that the compound or agent inhibits the expression of KSR ; and a ribozyme that cleaves KSR mRNA. (I) is useful for inhibiting the expression of mammalian KSR comprising contacting cells which express KSR with (I), where expression of mammalian KSR is inhibited. (I) is useful for conferring radiosensitivity to ionizing radiation in tumor cells in a mammal. (I) is useful for inhibiting angiogenesis in a mammal. (I) is useful for inhibiting or reducing VEGF expression or activity in a mammal. The methods are useful for treating or preventing hyperproliferative condition associated with expression of gf-Ras or heightened expression of Ras in a mammal and for treating or inhibiting the progression of cancer in a mammal. The cancer is chosen from

CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
 CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
 CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
 CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
 CC cancer. The present sequence represents a KSR antisense oligonucleotide.
 CC sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 other;
 CC

RESULT 5
 AEA46561/C
 ID AEA46561 standard; DNA; 18 BP.
 XX
 AC AEA46561;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ_ID NO:28.
 XX
 KW kinase suppressor of Ras; KSR; cytostatic; neoplasm; pancreas tumor;
 KW liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
 KW gastrointestinal disease; respiratory disease; genitourinary disease;
 KW endocrine disease; bladder tumor; colon tumor; intestine tumor;
 KW head & neck tumor; leukemia; hematological disease; lymphoma;
 KW immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 KW cardiovascular disease; antisense oligonucleotide; antisense therapy;
 KW prostate tumor; andrology; cancer; hyperproliferation;
 KW
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 PN WO2005056756-A2.
 XX
 DD 23-JUN-2005.
 XX
 PF 03-DEC-2004; 2004WO-US040506.
 XX
 PR 03-DEC-2003; 2003US-00727358.
 PA (SLOC) SLOAN KETTERING INST CANCER RES.
 PI Kolebscik RN, Xing HR;
 XX
 DR WPI; 2005-445165/45.
 XX
 PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 PT useful for inhibiting expression of mammalian KSR and treating
 PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.
 XX
 PS Claim 8; SEQ ID NO 28; 186pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) which is substantially
 CC complementary to a region of kinase suppressor of Ras (KSR) RNA, where
 CC the oligonucleotide inhibits the expression of KSR. Also included are the
 CC following: an oligonucleotide (II) which is substantially complementary
 CC to a translation initiation site, 5' untranslated region, coding region
 CC or 3' untranslated region of mRNA, encoding mammalian KSR; an antisense
 CC oligonucleotide (III) comprising a sequence substantially complementary
 CC to the 5' CAI region of KSR; an antisense oligonucleotide (IV) comprising a
 CC sequence substantially complementary to nucleotides 124-243 of the coding
 CC sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion;
 CC sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 other;
 CC

Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGGACCTAGAGGCAAG 18
 Db 1 CGGACCTAGAGGCAAG 18

CC an antisense oligonucleotide (V) comprising a sequence chosen from
 CC AR46539, AR46540 and AR46541, and a recombinant DNA molecule (VI),
 CC comprising a nucleic acid sequence which encodes on transcription an
 CC antisense RNA complementary to mammalian KSR RNA or its portion; a cell
 CC (VII) transfected with (VI); an expression vector (VII) capable of
 CC expressing a nucleic acid (VII) which is substantially complementary to the
 CC coding sequence of KSR RNA, or its portion/fragment, where the
 CC oligonucleotide/nucleic acid inhibits the expression of KSR; an
 CC expression vector (VII) capable of expressing an oligonucleotide which is
 CC substantially complementary to the CAI region of the coding sequence of
 CC KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the
 CC expression of KSR; a pharmaceutical composition (PCI), comprising (I) and
 CC a carrier or diluent; a composition (CI) comprising (I) and a carrier or
 CC diluent; a composition (C2) comprising one or more chemotherapeutic or
 CC radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA
 CC encoding mammalian KSR and which inhibits KSR expression; a composition
 CC (C3) comprising an expression vector and a carrier or diluent, where the
 CC expression vector is capable of expressing nucleic acid which is
 CC substantially complementary to the coding sequence of KSR RNA, or its
 CC portion/fragment, where the nucleic acid inhibits the expression of KSR RNA, or
 CC its portion/fragment, where the oligonucleotide which is substantially
 CC complementary to the coding sequence of KSR RNA, or its portion/fragment,
 CC cells which express KSR with a nucleic acid which is complementary to a
 CC portion of the mRNA encoding KSR; treating or preventing (M2) a
 CC hyperproliferative condition associated with the expression of Gf-Ras or
 CC heightened expression of Ras in a mammal comprising administering to the
 CC mammal a compound or agent which inhibits the expression of mammalian KSR
 CC protein; fragment, where the nucleic acid inhibits the expression of KSR RNA,
 CC associated with the expression of Gf-Ras or heightened expression of Ras
 CC in a mammal comprising expressing in the mammal or administering to the
 CC mammal therapeutically effective amount of a nucleic acid which is
 CC complementary to a portion of the mRNA encoding KSR; treating or
 CC inhibiting (M4) the progression of cancer in a mammal comprising
 CC administering to a mammal a compound or agent which inhibits the
 CC expression of mammalian KSR protein; inhibiting angiogenesis of tumor
 CC cells in a mammal, by administering to a mammal a compound or agent which
 CC inhibits the expression of mammalian KSR protein; inhibiting or reducing
 CC VEGF expression or activity in a mammal, by administering a compound or
 CC agent that inhibits the expression of mammalian KSR protein; stimulating
 CC angiogenesis in a mammal comprising administering to a mammal a
 CC therapeutically effective amount of a compound or agent which activates
 CC the expression of mammalian KSR protein or a vector expressing mammalian
 CC KSR; identifying compounds or agents which inhibit the expression of KSR,
 CC by incubating a cell expressing KSR in the presence and absence of a
 CC candidate compound or agent, and detecting or measuring the expression of
 CC KSR in the presence and absence of a candidate compound or agent, where a
 CC decrease in the expression of KSR in the presence of the candidate
 CC compound or agent versus in the absence of the candidate compound or
 CC agent indicates that the compound or agent inhibits the expression of KSR
 CC ; and a ribozyme that cleaves KSR mRNA. (I) Is useful for inhibiting the
 CC expression of mammalian KSR comprising contacting cells which express KSR
 CC with (I), where expression of mammalian KSR is inhibited. (I) Is useful for
 CC conferring radiosensitivity to ionizing radiation in tumor cells in a
 CC mammal. (I) Is useful for inhibiting angiogenesis in a mammal. (I) Is
 CC useful for inhibiting or reducing VEGF expression or activity in a
 CC mammal. The methods are useful for treating or preventing
 CC hyperproliferative condition associated with expression of Gf-Ras or
 CC heightened expression of Ras in a mammal and for treating or inhibiting
 CC the progression of cancer in a mammal. The cancer is chosen from
 CC pancreatic cancer, lung cancer, skin cancer, urinary tract cancer,
 CC bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal
 CC cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast
 CC cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate
 CC cancer. The present sequence represents a KSR antisense oligonucleotide.
 CC sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 CC

Query Match 100.0%; Score 18; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGGACCTAGAGGCAAG 18
 Db 1 CGGACCTAGAGGCAAG 1

KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the expression of KSR; a pharmaceutical composition (PC1) comprising (1) and a carrier or diluent; a composition (C2) comprising one or more chemotherapeutic or radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA encoding mammalian KSR and which inhibits KSR expression; a composition (C3) comprising an expression vector and a carrier or diluent, where the expression vector is capable of expressing nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the nucleic acid inhibit the expression of KSR; inhibiting (M1) the expression of mammalian KSR comprising contracting cells which express KSR with a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or preventing (M2) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising administering to the mammal a compound or agent which inhibits the expression of mammalian KSR protein; treating or preventing (M3) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising expressing in the mammal or administering to the mammal therapeutically effective amount of a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or inhibiting (M4) the progression of cancer in a mammal comprising administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting angiogenesis of tumor cells in a mammal, by administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting or reducing VEGF expression or activity in a mammal, by administering a compound or agent that inhibits the expression of mammalian KSR protein; stimulating angiogenesis in a mammal comprising administering to a mammal a therapeutically effective amount of a compound or agent which activates the expression of mammalian KSR protein, or a vector expressing mammalian KSR; identifying compounds or agents which inhibit the expression of KSR, by incubating a cell expressing KSR in the presence and absence of a candidate compound or agent, and detecting or measuring the expression of KSR in the presence and absence of a candidate compound or agent, where a decrease in the expression of KSR in the presence of the candidate compound or agent versus in the absence of the candidate compound or agent indicates that the compound or agent inhibits the expression of KSR; and a ribozyme that cleaves KSR mRNA. (1) Is useful for inhibiting the expression of mammalian KSR comprising contacting cells which express KSR with (1), where expression of mammalian KSR is inhibited. (1) Is useful for conferring radiosensitivity to tumor cells in a mammal. (1) Is useful for inhibiting angiogenesis in a mammal. (1) Is useful for inhibiting or reducing VEGF expression or activity in a mammal. The methods are useful for treating or preventing hyperproliferative condition associated with expression of gf-Ras or heightened expression of Ras in a mammal and for treating or inhibiting the progression of cancer in a mammal. The cancer is chosen from pancreatic cancer, lung cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate cancer. The present sequence represents a KSR antisense oligonucleotide.

RESULT 7																
ID	AE46558	Query Match	100.0%	Score	18	DB	14	Length	120							
XX	AE46558	Best Local Similarity	100.0%	Pred. No.	22											
AC		Matches	18	Conservative	0	Mismatches	0	Indels	0							
DT		Oy	1	CGGACCTAGAGGCAAG	18	Gaps	0									
		Db	91	CGGACCTAGAGGCAAG	108											
XX	SQ	Sequence	120	BP;	31	A;	36	C;	32	G;	21	T;	0	U;	0	Oster;

XX kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:25.
 KW kinase suppressor of Ras; KSR; cytostatic; neoplasm; pancreas tumor;
 KW liver tumor; skin tumor; thyroid tumor; lung tumor; urinary tract tumor;
 KW gastrointestinal disease; respiratory disease; genitourinary disease;
 KW endocrine disease; bladder tumor; colon tumor; intestinal tumor;
 KW head & neck tumor; hematologic disease; lymphoma;
 KW immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor; antiangiogenic;
 KW gynecology and obstetrics; ss; angiogenesis; disorder; antiangiogenic;
 KW cardiovascular disease; antisense oligonucleotide; antisense therapy;
 KW prostate tumor; andrology; cancer; hyperproliferation;
 XX OS Homo sapiens.
 OS mus sp.
 OS Synthetic.
 XX
 FH Location/Qualifiers
 FT Key 1 .120 a
 FT /tag= a
 FT /partial
 FT /product=. "kinase suppressor of Ras (KSR) fragment"
 FT /note= "No start or stop codon shown"
 XX WO2005056756-A2.
 XX PD 23-JUN-2005.
 XX 03-DEC-2004; 2004WO-US040506.
 XX 03-DEC-2003; 2003US-00727358.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Kolesnick RN, King HR,
 PI XX DR WII; 2005-445165145.
 DR p-PDB; AEA4659.
 XX New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression, useful for inhibiting expression of mammalian KSR and treating hyperproliferative conditions such as lung cancer, skin cancer, and ovarian cancer.
 XX Claim 6; SEQ ID NO 25; 186PP; English.
 CC The invention relates to an oligonucleotide (I) which is substantially complementary to a region of kinase suppressor of Ras (KSR) RNA, where the oligonucleotide inhibits the expression of KSR. Also included are the following: an oligonucleotide (II) which is substantially complementary to a translation initiation site, 5' untranslated region coding region to 3', untranslated region of mRNA encoding mammalian KSR; an antisense oligonucleotide (III) comprising a sequence substantially complementary to the CAL region of KSR; an antisense oligonucleotide (IV) comprising a sequence substantially complementary to nucleotides 124-243 of the coding sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion; an antisense oligonucleotide (V) comprising a sequence chosen from comprising a nucleic acid sequence which encodes on transcription an antisense RNA complementary to mammalian KSR RNA or its portion; a cell (VII) transfected with (VII); an expression vector (VII) capable of expressing a nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide/nucleic acid inhibits the expression of KSR; an expression vector (V2) capable of expressing an oligonucleotide which is substantially complementary to the CAL region of the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the expression of KSR RNA, or its portion/fragment, where the oligonucleotide/nucleic acid comprising (VII) and a carrier or diluent; a composition (C1) comprising (I) and a carrier or diluent; a composition (C2) comprising one or more chemotherapeutic or radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA encoding mammalian KSR and which inhibits KSR expression; a composition

KW intestine tumor; head & neck tumor; leukemia; hematological disease;
 KW lymphoma; immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 KW cardiovascular disease; antisense therapy; prostate tumor; andrology;
 KW cancer; hyperproliferation.
 XX Homo sapiens.
 XX OS
 PN WO2005056756-A2.
 PD 23-JUN-2005.
 PF 03-DEC-2004; 2004WO-US040506.
 XX PR 03-DEC-2003; 2003US-00727358.
 XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Kolesnick RN, Xing HR;
 XX DR WPI; 2005-445165/45.
 XX PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression,
 PT useful for inhibiting expression of mammalian KSR and treating
 PT hyperproliferative conditions such as lung cancer, skin cancer, and
 PT ovarian cancer.
 XX PS Example 5; SEQ ID NO 24; 186pp; English.

The invention relates to an oligonucleotide (I) which is substantially complementary to a region of kinase suppressor of Ras (KSR) RNA, where the oligonucleotide inhibits the expression of KSR. Also included are the following: an oligonucleotide (II) which is substantially complementary to a translation initiation site, 5' untranslated region, coding region or 3' untranslated region of mRNA encoding mammalian KSR; an antisense oligonucleotide (III) comprising a sequence substantially complementary to the CAl region of KSR; an antisense oligonucleotide (IV) comprising a sequence substantially complementary to nucleotides 124-243 of the coding sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion; an antisense oligonucleotide (V) comprising a sequence chosen from AEA46539, AEA46540 and AEA46541, and a recombinant DNA molecule (VI) comprising a nucleic acid sequence which encodes on transcription an antisense RNA complementary to mammalian KSR RNA or its portion; a cell (VII) transfected with (VI); an expression vector (VII) capable of expressing a nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide/nucleic acid inhibits the expression of KSR; an expression vector (VII) capable of expressing an oligonucleotide which is substantially complementary to the CAl region of the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the expression of KSR; a pharmaceutical composition (PC1) comprising (I) and a carrier or diluent; a composition (C1) comprising (I) and a carrier or diluent; a composition (C2) comprising one or more chemotherapeutic or radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA encoding mammalian KSR and which inhibits KSR expression; a composition (C3) comprising an expression vector and a carrier or diluent, where the expression vector is capable of expressing nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the nucleic acid inhibits the expression of KSR; cells which express KSR with a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or preventing (M2) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising administering to the mammal a compound or agent which inhibits the expression of mammalian KSR protein; treating or preventing (M3) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising expressing a mammal the amount of a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or preventing (M4) the progression of cancer in a mammal comprising administering to a mammal a compound or agent which inhibits the

expression of mammalian KSR protein; inhibiting angiogenesis of tumor cells in a mammal, by administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting or reducing VEGF expression or activity in a mammal, by administering a compound or agent that inhibits the expression of mammalian KSR protein; stimulating angiogenesis in a mammal comprising administering to a mammal a therapeutically effective amount of a compound or agent which activates the expression of mammalian KSR protein or a vector expressing mammalian KSR; identifying compounds or agents which inhibit the expression of KSR, by incubating a cell expressing KSR in the presence and absence of a candidate compound or agent, and detecting or measuring the expression of KSR in the presence and absence of a candidate compound or agent, where a decrease in the expression of KSR in the presence of the candidate compound or compound or agent versus in the absence of the candidate compound or agent indicates that the compound or agent inhibits the expression of KSR ; and a ribozyme that cleaves KSR mRNA. (I) Is useful for inhibiting the expression of mammalian KSR comprising contacting cells which express KSR with (I), where expression of mammalian KSR is inhibited. (I) Is useful for conferring radiosensitivity to ionizing radiation in tumor cells in a mammal. (I) Is useful for inhibiting angiogenesis in a mammal. (I) Is useful for inhibiting or reducing VEGF expression or activity in a mammal. The methods are useful for treating or preventing hyperproliferative condition associated with expression of gf-Ras or heightened expression of Ras in a mammal and for treating or inhibiting the progression of cancer in a mammal. The cancer is chosen from pancreatic cancer, lung cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate cancer. The present sequence represents human KSR1 cDNA.

CC XX SQ RESULT 9
 Sequence 2601 BP; 565 A; 818 C; 772 G; 446 T; 0 U; 0 Other;
 Query Match 100 %; Score 18; DB 14; Length 2601;
 Best Local Similarity 100 %; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CGGACCTTAGGGCAAG 18
 Db 187 CGGACCTTAGGGCAAG 204

RESULT 9
 ID AEA46544
 ID AEA46544 standard; cDNA; 4034 BP.
 XX AC AEA46544;
 XX DT 25-AUG-2005 (first entry)
 DE Mouse kinase suppressor of Ras (KSR) cDNA.
 XX KW gene; kinase suppressor of Ras; KSR; cytosolic; neoplasm;
 KW pancreas tumor; liver tumor; skin tumor; thyroid tumor; lung tumor;
 KW urinary tract tumor; gastrintestinal disease; respiratory disease;
 KW genitourinary disease; endocrine disease; bladder tumor; colon tumor;
 KW intestinal tumor; head & neck tumor; leukemia; hematological disease;
 KW lymphoma; immune disorder; esophagus tumor; breast tumor; stomach tumor;
 KW nervous system tumor; neurological disease; ovary tumor;
 KW gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic;
 KW cardiovascular disease; antisense therapy; prostate tumor; andrology;
 KW cancer; hyperproliferation.
 XX OS Mus sp.
 XX FH Key Location/Qualifiers
 FT 83..2704
 FT /*tag= a
 FT /product= "Mouse kinase suppressor of Ras (KSR)"
 XX PN WO2005056756-A2.
 PD 23-JUN-2005.

XX 03-DEC-2004; 2004WO-US040506.
 XX PR 03-DEC-2003; 2003US-00727358.
 XX PA (SLOC) SLOAN KETTERING INST CANCER RES.
 XX
 XX Kolencik RN, Xing HR;
 XX DR WPI; 2005-445155/45.
 XX DR P-PSDB; AEA46542.
 XX PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression, useful for inhibiting expressions of mammalian KSR and treating hyperproliferative conditions such as lung cancer, skin cancer, and ovarian cancer.
 XX PT Disclosure; SEQ ID NO 11; 18pp; English.
 XX
 CC The invention relates to an oligonucleotide (I) which is substantially complementary to a region of kinase suppressor of Ras (KSR) RNA, where the oligonucleotide inhibits the expression of KSR. Also included are the following: an oligonucleotide (II), which is substantially complementary to a translation initiation site, 5' untranslated region, coding region or 3' untranslated region of mRNA encoding mammalian KSR; an antisense oligonucleotide (III) comprising a sequence substantially complementary to the CA1 region of KSR; an antisense oligonucleotide (IV) comprising a sequence substantially complementary to nucleotides 124-243 of the coding sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion; an antisense oligonucleotide (V) comprising a sequence chosen from AEA46539, AEA46540 and AEA46541, and a recombinant DNA molecule (VI) comprising a nucleic acid sequence which encodes on transcription an substantially complementary to mammalian KSR RNA or its portion; a cell (VII) transfected with (VII); an expression vector (VII) capable of expressing a nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide/nucleic acid inhibits the expression of KSR; an expression vector (V2) capable of expressing an oligonucleotide which is substantially complementary to the CA1 region of the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the expression of KSR; a pharmaceutical composition (PCI) comprising (I) and a carrier or diluent; a composition (C1) comprising (I) and a carrier or diluent; a composition (C2) comprising one or more chemotherapeutic or radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA encoding mammalian KSR and which inhibits KSR expression; a composition (C3) comprising an expression vector and a carrier or diluent, where the expression vector is capable of expressing nucleic acid which is substantially complementary to the coding sequence of KSR RNA, or its portion/fragment, where the nucleic acid inhibits the expression of KSR; inhibiting (M1) the expression of mammalian KSR comprising contacting cells which express KSR with a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or preventing (M2) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising administering to the mammal a compound or agent which inhibits the expression of mammalian KSR protein; treating or preventing (M3) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising expressing gf-Ras or heightening expression of Ras in the mammal or diminishing to the mammal therapeutically effective amount of a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or inhibiting (M4) the progression of cancer in a mammal comprising administering to a mammal a compound or agent which inhibits angiogenesis of tumor cells in a mammal, by administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting or reducing VEGF expression or activity in a mammal, by administering a compound or agent that inhibits the expression of mammalian KSR protein; stimulating angiogenesis in a mammal comprising administering to a mammal a therapeutic amount of a compound or agent which activates the expression of mammalian KSR protein or a vector expressing mammalian KSR, identifying compounds or agents which inhibit the expression of KSR, by incubating a cell expressing KSR in the presence and absence of a candidate compound or agent, and detecting or measuring the expression of

CC protein kinase involved in the regulation of cell growth and differentiation. It was isolated from a mouse PCC4 teratocarcinoma cell line with a probe corresponding to hb, a sequence that had been identified as showing similarity to *Drosophila melanogaster Ksr* (see also AAT72154, CC AAT8216-57), have also been identified. These Ksr homologues define a novel class of kinases related to raf kinases. Ksr nucleic acids can be used to produce Ksr polypeptides, as probes to identify mutant Ksr alleles associated with disease, and in gene therapy applications

XX Sequence 4094 BP; 924 A; 1212 C; 1193 G; 765 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 4094;
Best Local Similarity 100.0%; Pred. No. 25; DB 12; Length 4094;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTCTAGAGGCCAAG 18
Db 296 CGGACCTCTAGAGGCCAAG 313

RESULT 11
ID ADG75394 standard; cDNA; 4094 BP.
XX ADG75394;
AC DT 11-MAR-2004 (first entry)
DE Mouse kinase suppressor of Ras (KSR) coding sequence.
KW antisense oligonucleotide; kinase suppressor of Ras; KSR; cancer; pancreatic cancer; lung cancer; skin cancer; urinary tract cancer; bladder cancer; liver cancer; thyroid cancer; colon cancer; intestinal cancer; breast cancer; ovarian cancer; stomach cancer; head cancer; neck cancer; oesophageal cancer; prostate cancer; leukaemia; lymphoma; neuroblastoma; mouse; murine; gene; ss.
XX OS Mus sp.
XX PN WO2003101396-A2.
PD 11-DEC-2003.
XX PR 29-MAY-2003; 2003WO-US016961.
XX PR 30-MAY-2003; 2003US-1384288P.
PR 03-APR-2003; 2003US-0460023P.
XX DR WPI; 2004-053335/05.
DR P-PSDB; ADG75392.

XX PT New antisense oligonucleotides complementary to a region of kinase suppressor of Ras (KSR) RNA which inhibit KSR expression, useful for treating or inhibiting progression of cancer, e.g. pancreatic, lung, skin, or bladder cancer.

PS Example 1; SEQ ID NO 11; 120PP; English.

CC The invention comprises antisense oligonucleotides which are designed to inhibit the expression of the kinase suppressor of Ras (KSR) gene. The antisense oligonucleotides of the invention are useful for treating or inhibiting the progression of cancer, such as: pancreatic cancer, lung cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal cancer, breast cancer, ovarian cancer, stomach cancer, head and neck cancer, oesophageal cancer, prostate cancer, leukaemia, lymphoma, and neuroblastoma. The present cDNA sequence encodes the mouse KSR protein.

CC Query Match 100.0%; Score 18; DB 12; Length 4094;
Best Local Similarity 100.0%; Pred. No. 25; DB 12; Length 4094;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTCTAGAGGCCAAG 18
Db 296 CGGACCTCTAGAGGCCAAG 313

RESULT 12
ID AEA46541/C
ID AEA46541 standard; DNA; 16 BP.
XX AEA46541;
AC DE Kinase suppressor of Ras (KSR) antisense oligonucleotide, SEQ ID NO:8.
XX Kinase suppressor of Ras: KSR; cyostatic; neoplasm; pancreatic tumor; gastrointestinal disease; respiratory disease; lung tumor; urinary tract tumor; liver tumor; skin tumor; thyroid tumor; genitourinary disease; endocrine disease; bladder tumor; colon tumor; intestine tumor; head & neck tumor; leukemia; hematological disease; lymphoma; immune disorder; esophagus tumor; neurological disease; breast tumor; stomach tumor; nervous system tumor; gynecology and obstetrics; ss; angiogenesis disorder; antiangiogenic; cardiovascular disease; antisense oligonucleotide; antisense therapy; prostate tumor; andrology; cancer; hyperproliferation.
XX OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX EN WO2005056756-A2.
XX PD 23-JUN-2005.
XX PR 03-DEC-2004; 2004WO-US040506.
XX PR 03-DEC-2003; 2003US-00727358.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Kolesnick RN, Xing HR;
DR WPI; 2005-445165/45.
XX PT New oligonucleotide inhibiting kinase suppressor of Ras (KSR) expression, useful for inhibiting expression of mammalian KSR and treating hyperproliferative conditions such as lung cancer, skin cancer, and ovarian cancer.

PS Claim 8; SEQ ID NO 8; 186pp; English.

CC The invention relates to an oligonucleotide (I) which is substantially complementary to a region of kinase suppressor of Ras (KSR) RNA where the oligonucleotide inhibits the expression of KSR. Also included are the following: an oligonucleotide (II) which is substantially complementary to a translation initiation site, 5' untranslated region, coding region or 3' untranslated region of mRNA encoding mammalian KSR; an antisense oligonucleotide (III) comprising a sequence substantially complementary to the 5' region of KSR; an antisense oligonucleotide (IV) comprising a sequence substantially complementary to nucleotides 124-243 of the coding sequence of mouse KSR or nucleotides 97-216 of human KSR or its portion; an antisense oligonucleotide (V) comprising a sequence chosen from AEA46539, AEA6540 and AEA46541, and; a recombinant DNA molecule (VI) comprising a nucleic acid sequence which encodes on transcription an antisense RNA complementary to mammalian KSR RNA or its portion; a cell (VII) transfected with (VI); an expression vector (VI) capable of expressing a nucleic acid which is substantially complementary to the

coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide/nucleic acid inhibits the expression of KSR; an expression vector (V2) capable of expressing an oligonucleotide which is substantially complementary to the CAL region of the coding sequence of KSR RNA, or its portion/fragment, where the oligonucleotide inhibits the expression of KSR; a pharmaceutical composition (C1) comprising (I) and a carrier or diluent; a composition (C2) comprising one or more chemotherapeutic or radiotherapeutic agent and an oligonucleotide which is targeted to a mRNA encoding mammalian KSR and which inhibits KSR expression; a composition (C3) comprising an expression vector and a carrier or diluent, where the expression vector is capable of expressing nucleic acid which is substantially complementary to the coding sequence of KSR, or its portion/fragment, where the nucleic acid inhibits the expression of KSR; cells which express KSR with a nucleic acid which is complementary to a portion of the mRNA encoding KSR; treating or preventing (M1) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising administering to the mammal a compound or agent which inhibits the expression of mammalian KSR protein; treating or preventing (M2) a hyperproliferative condition associated with the expression of gf-Ras or heightened expression of Ras in a mammal comprising administering to the mammal a compound or agent which inhibits the expression of gf-Ras or heightened expression of Ras in a mammal comprising administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting angiogenesis of tumor cells in a mammal, by administering to a mammal a compound or agent which inhibits the expression of mammalian KSR protein; inhibiting or reducing VEGF expression or activity in a mammal, by administering a compound or agent that inhibits the expression of mammalian KSR protein; stimulating angiogenesis in a mammal comprising administering to a mammal a therapeutically effective amount of a compound or agent which activates the expression of mammalian KSR protein or a vector expressing mammalian KSR; identifying compounds or agents which inhibit the expression of KSR, by incubating a cell expressing KSR in the presence and absence of a candidate compound or agent, and detecting or measuring the expression of KSR in the presence and absence of a candidate compound or agent, where a decrease in the expression of KSR in the presence of the candidate compound or agent indicates that the compound or agent inhibits the expression of KSR; and a ribozyme that cleaves KSR mRNA. (I) Is useful for inhibiting the expression of mammalian KSR comprising contacting cells which express KSR with (I), where expression of mammalian KSR is inhibited. (I) Is useful for conferring radiosensitivity to ionizing radiation in tumor cells in a mammal. (I) Is useful for inhibiting angiogenesis in a mammal. (I) Is useful for inhibiting or reducing VEGF expression or activity in a mammal. The methods are useful for treating or preventing hyperproliferative condition associated with expression of gf-Ras or heightened expression of Ras in a mammal and for treating or inhibiting the progression of cancer in a mammal. The cancer is chosen from pancreatic cancer, lung cancer, skin cancer, urinary tract cancer, bladder cancer, liver cancer, thyroid cancer, colon cancer, intestinal cancer, leukemia, lymphoma, neuroblastoma, head and neck cancer, breast cancer, ovarian cancer, stomach cancer, esophageal cancer and prostate cancer. The present sequence represents a KSR antisense oligonucleotide.

Sequence 16 BP; 1 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACCCCTAGAGGCAAG 18
Db 16 GACCCCTAGAGGCAAG 1

RESULT 13
ABL67488/C
ABL67488 Standard; DNA; 376 BP.
XX

AC ABL67488;

XX DT 15-MAY-2002 (first entry)

XX DE Thyroid cancer related gene sequence SEQ ID NO:5825.

XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.

XX OS Homo sapiens.

XX PN WO200194629-A2.

XX PD 13-DEC-2-2001.

XX PR 30-MAY-2001; 2001WO-US010838.

XX PR 05-JUN-2000; 2000US-0209473P.

XX PR 05-JUN-2000; 2000US-0209531P.

XX PR 18-SEP-2000; 2000US-0233113P.

XX PR 20-SEP-2000; 2000US-0233400P.

XX PR 20-SEP-2000; 2000US-0234024P.

XX PR 20-SEP-2000; 2000US-0234509P.

XX PR 22-SEP-2000; 2000US-0234567P.

XX PR 22-SEP-2000; 2000US-0234580P.

XX PR 25-SEP-2000; 2000US-0234923P.

XX PR 25-SEP-2000; 2000US-0234924P.

XX PR 25-SEP-2000; 2000US-0235082P.

XX PR 25-SEP-2000; 2000US-023513P.

XX PR 25-SEP-2000; 2000US-0235139P.

XX PR 25-SEP-2000; 2000US-0235280P.

XX PR 26-SEP-2000; 2000US-0235637P.

XX PR 26-SEP-2000; 2000US-0235638P.

XX PR 27-SEP-2000; 2000US-0235711P.

XX PR 27-SEP-2000; 2000US-0235720P.

XX PR 27-SEP-2000; 2000US-023584P.

XX PR 27-SEP-2000; 2000US-0236109P.

XX PR 28-SEP-2000; 2000US-0236111P.

XX PR 28-SEP-2000; 2000US-0236808P.

XX PR 28-SEP-2000; 2000US-0236832P.

XX PR 29-SEP-2000; 2000US-0236891P.

XX PR 29-SEP-2000; 2000US-0237172P.

XX PR 02-OCT-2000; 2000US-0237173P.

XX PR 02-OCT-2000; 2000US-0237278P.

XX PR 02-OCT-2000; 2000US-0237294P.

XX PR 02-OCT-2000; 2000US-0237295P.

XX PR 02-OCT-2000; 2000US-0237316P.

XX PR 03-OCT-2000; 2000US-0237422P.

XX PR 03-OCT-2000; 2000US-0237598P.

XX PR 03-OCT-2000; 2000US-0237608P.

XX PR 03-OCT-2000; 2000US-0237609P.

XX PR 01-NOV-2000; 2000US-0244678P.

XX PR 01-NOV-2000; 2000US-0245084P.

(AVAL-) AVALON PHARM.

PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

PI Soper DR, Weaver Z;

XX DR

XX PT Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

XX

PS Claim 1; SEQ ID NO 5825; 44pp; English.
 XX
 CC The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms tumour.
 CC Sequence 376 BP; 78 A; 132 C; 76 G; 90 T; 0 U; 0 other;
 CC Best Local Similarity 94.1%; Pred. No. 5.1e+02; 1; Mismatches 16; Conservative 0; Indels 0; Gaps 0;
 PR SQ
 Query Match 85.6%; Score 15.4; DB 6; Length 376;
 PR Best Local Similarity 94.1%; Pred. No. 5.1e+02; 1; Mismatches 16; Conservative 0; Indels 0; Gaps 0;
 PR Db 107 GGACCTAGAGGCAAG 18
 PR AC ABL69201;
 PR XX
 PR DT 15-MAY-2002 (first entry)
 PR DE Prostate cancer related gene sequence SEQ ID NO:7538.
 PR XX
 PR Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytotoxic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma; gene; ds.
 PR XX
 PR OS Homo sapiens.
 PR XX
 PR EN WO200194629-A2.
 PR XX
 PR PD 13-DEC-2001.
 PR XX
 PR PF 30-MAY-2001; 2001WO-US010838.
 PR XX
 PR 05-JUN-2000; 2000US-0209473P.
 PR PR 05-JUN-2000; 2000US-0209531P.
 PR PR 18-SEP-2000; 2000US-023313P.
 PR PR 20-SEP-2000; 2000US-023361P.
 PR PR 20-SEP-2000; 2000US-0234009P.
 PR PR 20-SEP-2000; 2000US-0234034P.
 PR PR 20-SEP-2000; 2000US-0234052P.
 PR PR 22-SEP-2000; 2000US-0234509P.
 PR PR 22-SEP-2000; 2000US-0234567P.
 PR PR 25-SEP-2000; 2000US-0234933P.
 PR PR 25-SEP-2000; 2000US-0234934P.
 PR PR 25-SEP-2000; 2000US-0235077P.
 PR PR 25-SEP-2000; 2000US-0235082P.
 PR PR 25-SEP-2000; 2000US-0235134P.
 PR PR 26-SEP-2000; 2000US-0235209P.
 PR PR 26-SEP-2000; 2000US-0235637P.
 PR PR 27-SEP-2000; 2000US-0235638P.
 PR PR 27-SEP-2000; 2000US-0235711P.
 PR PR 27-SEP-2000; 2000US-0235720P.
 PR PR 28-SEP-2000; 2000US-0236028P.
 PR PR 28-SEP-2000; 2000US-0236032P.
 PR PR 28-SEP-2000; 2000US-0236033P.
 PR PR 28-SEP-2000; 2000US-0236034P.
 PR PR 28-SEP-2000; 2000US-0236109P.
 PR PR 28-SEP-2000; 2000US-0236111P.
 PR PR 21-SEP-2000; 2000US-0236842P.
 PR PR 21-SEP-2000; 2000US-0236891P.
 PR PR 02-OCT-2000; 2000US-0237172P.
 PR PR 02-OCT-2000; 2000US-0237278P.
 PR PR 03-OCT-2000; 2000US-0237604P.
 PR PR 02-OCT-2000; 2000US-0237294P.
 PR PR 03-OCT-2000; 2000US-0237295P.
 PR PR 03-OCT-2000; 2000US-0237316P.
 PR PR 03-OCT-2000; 2000US-0237425P.
 PR PR 03-OCT-2000; 2000US-0237598P.
 PR PR 03-OCT-2000; 2000US-0237604P.
 PR PR 03-OCT-2000; 2000US-0237606P.
 PR PR 03-OCT-2000; 2000US-0237608P.
 PR PR 01-NOV-2000; 2000US-0244867P.
 PR PR 01-NOV-2000; 2000US-0245084P.
 PR PA (AVAL-) AVALON PHARM.
 PR XX
 PR Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PR Soppe DR, Weaver Z;
 PR XX
 PR DR WPI; 2002-188264/24.
 PR PT Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
 PR XX
 PR GS
 PS Claim 1; SEQ ID NO 7538; 44pp; English.
 PS CC The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.
 PS XX
 PS SQ Sequence 376 BP; 78 A; 132 C; 76 G; 90 T; 0 U; 0 other;
 PS Query Match 85.6%; Score 15.4; DB 6; Length 376;
 PS PR Best Local Similarity 94.1%; Pred. No. 5.1e-02; 1; Mismatches 16; Conservative 0; Indels 0; Gaps 0;
 PS PR Db 107 GGACCTAGAGGCAAG 18
 PS PR AC ADF80786;
 PS PR XX
 PS DT 26-FEB-2004 (first entry)

XX
DR Leukaemia-related DNA sequence #1342.
XX
KW Cytostatic; Gene therapy; leukaemia; ss.
XX
OS Unidentified.
XX
WO2003039443-A2.
XX
PD 15-MAY-2003.
XX
PP 04-NOV-2002; 2002WO-EP012303.
XX
PR 05-NOV-2001; 2001EP-00156244.
PR 30-APR-2002; 2002EP-00009758.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFFE-) HAFFERLACH T.
PA (SCHO-) SCHOCH C.
PA (KERN/) KERN W.
XX
PI Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
PI Eils R, Brorb B, Mergenthaler S;
XX
DR WPI; 2003-505037/47.
XX
PS Disclosure; SEQ ID NO 1342; 2938pp; English.
XX
CC The present invention relates to a method (M1) for determining the
CC subtype of leukaemia cells and whether a patient sample contains
CC leukaeimia cells. The method comprises determining the expression profile
CC of a group of markers in a patient sample. The method is useful for
CC determining the presence of leukaemia cells, its types or subtypes, and
CC for the preparation of a medicament for treating leukaemia.
XX
SQ Sequence 388 BP; 119 A; 91 C; 57 G; 121 T; 0 U; 0 Other;
Query Match 85.6%; Score 15.4; DB 10; Length 388;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACCTTAGGGCAAG 18
Db 360 GGACCTTAGGGCAAG 344

RESULT 16
AAK8398/C
ID AAK8398 standard; cDNA; 514 BP.
XX
AC AAK8398;
XX
DT 05-NOV-2001 (first entry)
DE Human digestive system antigen coding sequence SEQ ID NO: 714.
XX
Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ss.
XX
OS Homo sapiens.
XX
WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PP 17-JAN-2001; 2001WO-US001324.

PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-024121P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 01-NOV-2000; 2000US-024168P.
 PR 08-NOV-2000; 2000US-0244674P.
 PR 08-NOV-2000; 2000US-0244675P.
 PR 08-NOV-2000; 2000US-0244677P.
 PR 08-NOV-2000; 2000US-0244678P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246529P.
 PR 08-NOV-2000; 2000US-0246603P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-024925P.
 PR 17-NOV-2000; 2000US-0249259P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 01-DEC-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250291P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251836P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251899P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 PT WPI; 2001-502630/55.
 DR P-PSDB; AAM92625.
 PR Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases.
 XX
 RS Claim 1; SEQ ID NO 714; 986pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including, cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a cDNA encoding a digestive
 CC system antigen of the invention
 XX
 SQ Sequence 514 BP; 162 A; 115 C; 96 G; 141 T; 0 U; 0 Other;
 Query Match 85.6%; Score 15.4; DB 4; Length 514;
 Best Local Similarity 94.1%; Pred. No. 5.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GGACCCTAGAGGCAANG 18
 DB 430 GGACCTTAGAGGCCAAG 414

PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0223447P.
 PR 14-AUG-2000; 2000US-0223757P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-022668P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-022824P.
 PR 01-SEP-2000; 2000US-0228287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 08-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0233398P.
 PR 14-SEP-2000; 2000US-0233499P.
 PR 14-SEP-2000; 2000US-0233401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 27-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 08-NOV-2000; 2000US-0244809P.
 PR 08-NOV-2000; 2000US-0244826P.
 PR 08-NOV-2000; 2000US-0244817P.
 PR 08-NOV-2000; 2000US-0244674P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-Nov-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246522P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-024907P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 01-DEC-2000; 2000US-025016P.
 PR 01-DEC-2000; 2000US-0250394P.
 PR 05-DEC-2000; 2000US-0251010P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-025186P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-025199P.
 PR 11-DEC-2000; 2000US-025409P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;
 PT XX WPI; 2001-465567/5.
 DR P-PSDB; AAU22619.

XX PT Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon including colon cancers and also for testing and detection e.g. diagnosis.

XX PS Claim 4; SEQ ID NO 162; 562pp; English.

CC The present invention relates to the isolation of novel human colon associated polypeptides (AAU22468-AAU22701), and the cDNA and genomic sequences encoding for them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders of the colon including colon cancer, congenital anomalies (e.g. atresia and stenosis), bacterial and viral infections, inflammatory bowel disease (IBD), neoplastic cell disorders (e.g. polyps and adenomas, intestinal inflammatory disorders, colitis, colonic inflammation, diarrhoea and dysentery, malabsorption syndromes (e.g. lactose intolerance), intestinal obstruction and sigmoid diseases). The polynucleotides sequences of the invention can also be used in gene therapy. AAU33188-AAU33181 represent cDNA sequences encoding for the novel human colon associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 514 BP; 162 A; 115 C; 96 G; 141 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 5; Length 514;
 Best Local Similarity 94.1%; Pred. No. 5_1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX
 PS Example 2; SEQ ID NO 7641; 210pp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual,
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC DNA of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 1797 BP; 574 A; 340 C; 360 G; 523 T; 0 U; 0 Other;
 Query Match 85.6%; Score 15.4; DB 12; Length 1797;
 Best Local Similarity 94.1%; Pred. No. 5.3e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 GGACCTTAGAGGAAAG 18
 Db 502 GGACCTAGAGGAAAG 486

RESULT 21
 ADQ18079
 ID ADQ18079 Standard; DNA; 9645 BP.
 XX
 AC ADQ18079;
 DT 26-AUG-2004 (first entry)
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 896.
 XX
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW db.
 OS Homo sapiens.
 XX
 WO2004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 PR 26-NOV-2003; 2003WO-US038193.
 XX
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Aziz N, Ginsburg WM, Zlotnik A;
 XX
 DR WPI; 2004-441208/41.
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT barcoma.
 XX
 PS Example 2; SEQ ID NO 896; 210pp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual,
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC

CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC DNA of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 9645 BP; 2115 A; 2895 C; 2715 G; 1920 T; 0 U; 0 Other;
 Query Match 85.6%; Score 15.4; DB 12; Length 9645;
 Best Local Similarity 94.1%; Pred. No. 5.3e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 GGACCTAGAGGAAAG 18
 Db 319 GGACCCGGAGGAAAG 335

RESULT 22
 AD259509/c
 ID AD259509 Standard; DNA; 20001 BP.
 XX
 AC AD259509;
 DT 30-JUN-2005 (first entry)
 DE Secondary hyperparathyroidism detection human polymorphic gene, CHI3L1.
 XX
 KW secondary hyperparathyroidism; endocrine-gen.; antithyroid;
 KW renal failure; nephropathic; SNP detection;
 KW single nucleotide polymorphism; SNP; gene; ds; CHI3L1.
 XX
 OS Homo sapiens.
 XX
 PT variation /standard_name= "Single nucleotide polymorphism"
 PT
 PN JP2005102601-A.
 XX
 PR 21-APR-2005.
 XX
 PR 30-SEP-2003; 2003JP-00341015.
 XX
 PA (HYUB-) HYURITTO GENOMICS KK.
 PA (JIKE-) UNIV JIKEI.
 XX
 PR 2005-358641/37.
 XX
 PT Testing secondary hyperparathyroidism in chronic renal failure patient,
 PT involves detecting variation in gene chosen from CACNA1C, CALCR, CHI3L1,
 PT EGF, FGFR1, GPR56 and GPRK6.
 XX
 PS Claim 4; SEQ ID NO 3; 138pp; Japanese.
 XX
 PT The invention relates to a novel method for testing secondary
 CC hyperparathyroidism in a chronic renal failure patient. The method
 CC involves detecting a variation in a gene chosen from CACNA1C, CALCR, CHI3L1,
 CC CHI3L1, EGR1, GPR56, GPRK6, IL10RA, IL10RB, IL12B1, KCNQ14,
 CC KCNQ1, ORC1L4, PDGFRA, SCYB14, SLC12A1, SLC23, TGFBR3, TMEM1, CALCR,
 CC IL17R, OSF1, FGFR6, HGF, MET, TGFB1 and VEGF, or detecting the base in a
 CC polymorphism region existing in the vicinity of any one of the genes. The
 CC invention further comprises a reagent or kit for testing secondary
 CC hyperparathyroidism in a chronic renal failure patient. This
 CC polynucleotide sequence represents the polymorphism containing human
 CC CHI3L1 gene of the invention.
 XX
 SQ Sequence 20001 BP; 4773 A; 5041 C; 5158 G; 5029 T; 0 U; 0 Other;
 Query Match 85.6%; Score 15.4; DB 14; Length 20001;
 Best Local Similarity 94.1%; Pred. No. 5.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FH Key Location/Qualifiers
FT CDS 1. .191150
FT /tag= b
FT /product= "Human platelet derived growth factor receptor
FT alpha wild-type protein"
FT exon 1. .49
FT /tag= a
FT number= 1
FT intron 50..2330
FT /tag= c
FT /number= 1
FT exon 2331..2648
FT /tag= d
FT /number= 2
FT intron 2649..4902
FT /tag= e
FT /number= 2
FT exon 4903..5163
FT /tag= f
FT /number= 3
FT intron 5164..6154
FT /tag= g
FT /number= 3
FT exon 6155..6285
FT /tag= h
FT /number= 4
FT intron 6286..8524
FT /tag= i
FT /number= 4
FT exon 8325..8696
FT /tag= j
FT /number= 5
FT intron 8697..8787
FT /tag= k
FT /number= 5
FT exon 8788..8977
FT /tag= l
FT /number= 6
FT intron 8978..166510
FT /tag= m
FT /number= 6
FT exon 166511..166526
FT /tag= n
FT /number= 7
FT intron 166627..168271
FT /tag= o
FT /number= 7
FT exon 168272..168398
FT /tag= p
FT /number= 8
FT intron 168399..169414
FT /tag= q
FT /number= 8
FT exon 169415..169608
FT /tag= r
FT /number= 9
FT intron 169609..170408
FT /tag= s
FT /number= 9
FT exon 170409..170503
FT /tag= t
FT /number= 10
FT intron 170504..170718
FT /tag= u
FT /number= 10
FT exon 170719..170851
FT /tag= v
FT /number= 11
FT intron 170852..17265
FT /tag= w
FT /number= 11
FT exon 173266..173370
FT /tag= x

SQ Query Match 85.6%; Score 15.4; DB 12; Length 22475;
Best Local Similarity 94.1%; Pred. No. 5.8e+02;
Matches 16; **Conservative** 0; **Mismatches** 1; **Indels** 0; **Gaps** 0;

OY 2 GGACCCCTAGAGCCAAG 18
Db 15390 GGACCCCTAGAGGAAG 15374

RESULT 24
ID ADM69029
AC ADM69029;
XX
DT 03-JUN-2004 (first entry)
DE Human platelet derived growth factor receptor alpha wild-type gDNA.
XX platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW wild-type; type III receptor tyrosine kinase; RTK; ds; gene.
XX Homo sapiens.
OS

FT intron /number= 12
 FT 173371. .173773
 FT /*tag= Y
 FT /number= 12
 FT 173774. .173884
 FT /*tag= Z
 FT /number= 13
 FT /*tag= aa
 FT /number= 13
 FT 174240. .174393
 FT /*tag= ab
 FT /number= 14
 FT 174394. .176193
 FT /*tag= ac
 FT /number= 14
 FT 176194. .176360
 FT /*tag= ad
 FT /number= 15
 FT 176361. .181248
 FT /*tag= ae
 FT /number= 15
 FT 181249. .181364
 FT /*tag= af
 FT /number= 16
 FT 181365. .181718
 FT /*tag= ag
 FT /number= 15
 FT 181719. .181841
 FT /*tag= ah
 FT /number= 17
 FT 181842. .183307
 FT intron /*tag= ai
 FT exon 183308. .183419
 FT /*tag= aj
 FT /number= 18
 FT 183420. .184676
 FT /*tag= ak
 FT /number= 18
 FT 184677. .184776
 FT /*tag= al
 FT /number= 19
 FT 184777. .184886
 FT /*tag= am
 FT /number= 19
 FT 184887. .184992
 FT /*tag= an
 FT /number= 20
 FT 184993. .186190
 FT /*tag= aq
 FT /number= 20
 FT 186191. .186432
 FT /*tag= ap
 FT /number= 21
 FT 186433. .191002
 FT /*tag= aq
 FT /number= 21
 FT 191003. .191150
 FT /*tag= ar
 FT /number= 22
 PN W02003105773-A2.
 PD 24-DEC-2003.
 XX 13-JUN-2003; 2003WO-US018901.
 PR 13-JUN-2002; 2002US-0389107P.
 PR 08-JAN-2003; 2003US-0438899P.
 PA (UYOR-) UNIV OREGON HEALTH SCI
 PA (DAND) DANA FARBER CANCER INSTI INC.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (USCO) US DEPT VETERANS AFFAIRS.
 XX Heinrich MC, Corless CL, Fletcher JA, Demetri GD;
 DR DR; ADM69012.
 XX P-PSDB; P-PSDB; ADM69012.
 PS Example 1; SEQ ID NO 19; 302pp; English.
 XX New isolated variant platelet derived growth factor alpha (PDGFR α) polypeptide, useful for screening for a compound useful in influencing PDGFR α -mediated neoplasia in a mammal.
 PT Sequence 191150 BP; 55223 A; 39036 C; 39352 G; 56412 T; 0 U; 1127 Other;
 CC The invention relates to a novel isolated variant platelet derived growth factor receptor-alpha (PDGFR α) polypeptide. The polypeptide of the invention is a type III receptor tyrosine kinase (RTK) and may be useful for screening for a compound that may influence PDGFR α -mediated neoplasia in a mammal. The current sequence is that of the human PDGFR α wild-type genomic DNA of the invention.
 CC Sequence 191150 BP; 55223 A; 39036 C; 39352 G; 56412 T; 0 U; 1127 Other;
 CC Query Match 85.6%; Score 15.4%; DB 12; Length 191150;
 CC Best Local Similarity 94.1%; Pred. No. 6.2e+02;
 CC Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC QY 2 GGACCTTGAGGCAAG 18
 DB 117726 GGACCCAGAGGAAG 117742
 RESULT 25
 ABZ07598 ID ABZ07598 standard; DNA; 50 BP.
 XX AC ABZ07598;
 XX DT 09-JAN-2003 (first entry)
 XX DE Human leukocyte gene expression profiling probe SEQ ID NO 7589.
 XX KW T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.
 XX OS Homo sapiens.
 XX PN W020057414-A2.
 XX PD 25-JUL-2002.
 XX PR 22-OCT-2001; 2001WO-US047956.
 XX PR 20-OCT-2000; 2000US-0241994P.
 XX PR 08-JUN-2001; 2001US-0296764P.
 XX PA (BIOC-) BIOCARDIA INC.
 PR Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PR LY N, Woodward R, Quertermous T, Johnson F;
 XX DR WPI; 2002-636525/68.
 XX New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
 XX Claim 1; Page 572; Opp; English.
 CC The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a

gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ00152) each having 50 base pairs (bp). The system is useful

for leukocyte expression profiling. It is particularly useful for diagnosing a disease; monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus,

rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX sequence 50 BP; 12 A; 15 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTTAGGGCAA 16
Db 18 GGACCTTAGGGCAA 32

RESULT 26
ADP10220
ID ADP10220 standard; DNA; 50 BP.

XX
AC ADP10220;
XX

DT 12-AUG-2004 (first entry)
DE 50-mer oligonucleotide marker probe of the invention #229.

DE 50-mer oligonucleotide marker probe of the invention #229.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;

KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.

XX
PD 21-MAY-2004.
XX
PP 24-APR-2003; 2003WO-US012946.

XX
PR 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX
PI Wohlgemuth, J.; Fry, K.; Woodward, R.; Ly, N.; Prentice, J.; Morris, M.;
PI Rosenberg, S.;
XX
DR WPI; 2004-400724/37.

XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.

XX
PT the genes.

PS Claim 2; SEQ ID NO 229; 1762pp; English.

XX
CC The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual

CC comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic

CC islet, lung, bone marrow or stem cell transplant rejection, in an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or

CC 50 mer oligonucleotide marker for diagnosis and monitoring of allograft

CC rejection and other disorders.

CC XX Sequence 50 BP; 12 A; 15 C; 11 G; 12 T; 0 U; 0 Other;

CC SQ Query Match 83.3%; Score 15; DB 12; Length 50;
CC Best Local Similarity 100.0%; Pred. No. 7.6e+02; Mismatches 0; Indels 0; Gaps 0;

CC QY 2 GGACCTTAGGGCAA 16
CC Db 18 GGACCTTAGGGCAA 32

RESULT 27
AAT76987/C

CC ID AA176987 standard; DNA; 51 BP.

CC AC AAT76987;
CC DT 09-NOV-2001 (first entry)

CC DE Human silent SNP containing nucleic acid SEQ:3928.
CC KW Human; single nucleotide polymorphism; SNP; genome; gene therapy; protein therapy; vaccine; diagnostic assay; detection; quantitation; restorative therapy; polymorphic; ds.

CC OS Homo sapiens.
CC XX PN WO20140521-A2.

CC XX PD 07-JUN-2001.

CC XX PR 30-NOV-2000; 2000WO-US032758.

CC XX PR 30-NOV-1999; 99US-0181382.

CC XX PR 29-NOV-2000; 2000US-00726173.

CC PA (CURA-) CURAGEN CORP.

CC XX PI Shinketsu, RA; Leach, M;

CC XX DR WPI; 2001-356160/37.

CC XX PT Polymorphic nucleic acid sequences, useful in genetic testing and therapy.

CC XX PS Claim 1; Page 1254; 2653pp; English.

CC XX CC AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC CC AAM53114 to AAM53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own

CC production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of corrective therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples

CC XX Sequence 51 BP; 9 A; 12 C; 19 G; 11 T; 0 U; 0 Other;

CC SQ Query Match 83.3%; Score 15; DB 4; Length 51;

CC Best Local Similarity 100.0%; Pred. No. 7.6e+02;

Matches	15;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	GGACCTAGAGGCAA	16						RESULT 29
ID									ABQ95689
Db	17	GGACCTAGAGGCAA	3						ID ABQ95689 standard; DNA; 75 BP.
									XX
									AC ABQ95689;
									XX
									DT 28-OCT-2002 (first entry)
									XX
									DE Tumour suppression-related oligonucleotide #11340.
									XX
									KW Tumour; cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; human;
									KW tumour suppression; tumour reversion; apoptosis; viral resistance;
									KW viral infection; cell degeneration disease; neurodegeneration; ds;
									KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
									OS Homo sapiens.
									XX
									PN FR2819824-A1.
									XX
									PD 26-JUL-2002.
									XX
									PF 23-JAN-2001; 2001FR-00000899.
									XX
									PR 23-JAN-2001; 2001FR-00000899.
									XX
									PA (MOLE-) MOLECULAR ENGINES LAB SA.
									XX
									PT Teferman A., Amson R., Tuijnder M., Susini L;
									XX
									DR WPI; 2002-610803/66.
									XX
									XX
									PT New nucleic acid implicated e.g. in tumor suppression, useful for
									PT diagnosis of tumors, viral infection and cellular degeneration and for
									PT drug screening.
									XX
									PS Claim 1; Page 375; 623pp; French.
									XX
									CC The present invention relates to novel human nucleic acid sequences (I).
									CC The present sequence is one such nucleic acid sequence. Expression of (I)
									CC are implicated in tumour suppression or reversion and apoptosis and viral
									CC resistance. (I) are useful as probes or primers for detecting,
									CC identifying, measuring and/or amplifying nucleic acid sequences, as
									CC antisense reagents and for recombinant production of polypeptides. (I)
									CC polypeptides (II) encoded by (I), vector containing (I), cells containing
									CC these vectors and antibodies (Rb) against (II) are all useful for
									CC treatment/prevention of viral, tumor and cell degeneration diseases
									CC (especially neurodegeneration, such as Alzheimer's disease and
									CC schizophrenia). Analysing the expression of (I) is also useful for
									CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying
									CC (I) are used for studying the aetiology of these diseases (also immune
									CC and inflammatory diseases). Note: In the present specification, SEQ ID 1
									CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
									CC in the specification
									XX
									SQ Sequence 75 BP; 27 A; 12 C; 19 G; 17 T; 0 U; 0 Other;
									Query Match 83.3%; Score 15; DB 4; Length 51;
									Best Local Similarity 100.0%; Pred. No. 7.6e+02;
									Mismatches 15; Conservative 0; Indels 0; Gaps 0;
									RESULT 30
									ACG24825
									ID ACG24825 standard; cDNA; 163 BP.
									XX
									AC ACG24825;
									XX
									DT 09-OCT-2000 (first entry)

XX
DE Human secreted protein 5' EST, SEQ ID NO: 28900.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PP 21-FEB-2000; 2000EP-00200610.
XX PR 26-FEB-1999; 99US-0122487P.
XX PA (GEST) GENSET.
XX PI Dumas Mine Edwards J, Duclert A, Giordano J;
XX DR WPI; 2000-500381/45.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 1; SEQ ID NO 28900; 71PP + Sequence Listing; English.
XX CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3', untranslated region (UTR)
CC of the mRNA, because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX SQ Sequence 163 BP; 35 A; 57 C; 41 G; 30 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 3; Length 163;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	GGACCTTAGAGCAA	16
Db	148	GGACCTTAGAGCAA	162

Search completed: April 15, 2006, 20:26:40
Job time : 692 Secs

OM nucleic - nucleic search, using sw model											
Copyright (c) 1993 - 2006 Biocceleration Ltd.											
Run on: April 15, 2006, 18:12:40 ; Search time 418 Seconds (Without alignments) 173.447 Million cell updates/sec											
Title: US-10-727-358-5											
Perfect score: 18											
Sequence: 1 cggacccataggccaag 18											
Scoring table: IDENTITY_NUC											
Gapop 1.0 , Gapext 1.0											
Searched: 9281099 seqs, 2013915447 residues											
Total number of hits satisfying chosen parameters: 18562198											
Minimum DB seq length: 0											
Maximum DB seq length: 200000000											
Post-processing: Maximum Match 0% Maximum Match 100% Listing first 300 summaries											
Database : Published Applications NA_New,*											
1:	/SIDSS5/podata/2/pupnna/US08	NEW	PUB	seq:	*	c	19	15.4	85.6	8703	
2:	/SIDSS5/podata/2/pupnna/US06	NEW	PUB	seq:	*	c	20	15.4	85.6	8703	
3:	/SIDSS5/podata/2/pupnna/US07	NEW	PUB	seq:	*	c	21	15.4	85.6	22475	
4:	/SIDSS5/podata/2/pupnna/PCT	NEW	PUB	seq:	*	c	22	15.4	85.6	100000	
5:	/SIDSS5/podata/2/pupnna/US09	NEW	PUB	seq:	*	c	23	15.4	85.6	171732	
6:	/SIDSS5/podata/2/pupnna/US05	NEW	PUB	seq:	*	c	24	15	83.3	19	
7:	/SIDSS5/podata/2/pupnna/US10	NEW	PUB	seq:	*	c	25	15	83.3	12	
8:	/SIDSS5/podata/2/pupnna/US10	NEW	PUB	seq:	*	c	26	15	83.3	19	
9:	/SIDSS5/podata/2/pupnna/US11	NEW	PUB	seq2:	*	c	27	15	83.3	19	
10:	/SIDSS5/podata/2/pupnna/US10	NEW	PUB	seq3:	*	c	39	14.8	82.2	594	
11:	/SIDSS5/podata/2/pupnna/US11	NEW	PUB	seq:	*	c	40	14.8	82.2	594	
12:	/SIDSS5/podata/2/pupnna/US11	NEW	PUB	seq2:	*	c	41	14.8	82.2	594	
13:	/SIDSS5/podata/2/pupnna/US11	NEW	PUB	seq3:	*	c	42	14.8	82.2	600	
14:	/SIDSS5/podata/2/pupnna/US11	NEW	PUB	seq4:	*	c	43	14.8	82.2	600	
15:	/SIDSS5/podata/2/pupnna/US60	NEW	PUB	seq:	*	c	44	14.8	82.2	600	
Pred. No.: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
Result	Query No.	Score	Match Length	DB ID	Description	c	19	15.4	85.6	8703	
1	15.4	85.6	539	9	US-10-301-480-55145	Sequence 55145, A	c	20	15.4	85.6	8703
2	15.4	85.6	539	10	US-10-301-480-668554	Sequence 688554,	c	21	15.4	85.6	22475
3	15.4	85.6	574	6	US-09-925-5025-065A-504327	Sequence 504327,	c	22	15.4	85.6	100000
4	15.4	85.6	738	6	US-09-925-065A-65294	Sequence 65294, A	c	23	15.4	85.6	171732
5	15.4	85.6	738	6	US-09-925-065A-65295	Sequence 65295, A	c	24	15	83.3	19
6	15.4	85.6	738	6	US-09-925-065A-65296	Sequence 65296, A	c	25	15	83.3	12
7	15.4	85.6	738	9	US-10-301-480-166533	Sequence 166533,	c	26	14.4	80.0	454
8	15.4	85.6	738	9	US-10-301-480-166534	Sequence 166534,	c	27	14.4	80.0	454
9	15.4	85.6	738	9	US-10-301-480-166535	Sequence 166535,	c	28	14.4	80.0	568
10	15.4	85.6	738	10	US-10-301-480-779943	Sequence 779943,	c	29	15	83.3	19
11	15.4	85.6	738	10	US-10-301-480-779943	Sequence 779944,	c	30	15	83.3	12
12	15.4	85.6	1155	8	US-10-750-185-61166	Sequence 61166, A	c	31	15	83.3	19
13	15.4	85.6	1155	8	US-10-750-62-61166	Sequence 61166, A	c	32	15	83.3	19
14	15.4	85.6	1206	9	US-10-932-182A-2596	Sequence 2596, AP	c	33	15	83.3	22
15	15.4	85.6	1206	9	US-10-932-182A-2596	Sequence 2596, AP	c	34	14.8	82.2	594
16	15.4	85.6	1806	11	US-11-932-182A-2596	Sequence 33575, A	c	35	14.8	80.0	584
17	15.4	85.6	1806	11	US-11-932-182A-2596	Sequence 33575, A	c	36	14.8	80.0	584
18	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	37	14.8	80.0	584
19	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	38	14.8	80.0	584
20	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	39	14.8	80.0	584
21	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	40	14.8	80.0	584
22	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	41	14.8	80.0	584
23	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	42	14.8	80.0	584
24	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	43	14.8	80.0	584
25	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	44	14.8	80.0	584
26	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	45	14.8	80.0	584
27	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	46	14.8	80.0	584
28	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	47	14.8	80.0	584
29	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	48	14.8	80.0	584
30	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	49	14.8	80.0	584
31	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	50	14.8	80.0	584
32	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	51	14.8	80.0	584
33	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	52	14.8	80.0	584
34	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	53	14.8	80.0	584
35	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	54	14.8	80.0	584
36	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	55	14.8	80.0	584
37	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	56	14.8	80.0	584
38	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	57	14.8	80.0	584
39	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	58	14.8	80.0	584
40	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	59	14.8	80.0	584
41	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	60	14.8	80.0	584
42	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	61	14.8	80.0	584
43	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	62	14.8	80.0	584
44	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	63	14.8	80.0	584
45	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	64	14.8	80.0	584
46	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	65	14.8	80.0	584
47	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	66	14.8	80.0	584
48	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	67	14.8	80.0	584
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50	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	69	14.8	80.0	584
51	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	70	14.8	80.0	584
52	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	71	14.8	80.0	584
53	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	72	14.4	80.0	454
54	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	73	14.4	80.0	454
55	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	74	14.4	80.0	454
56	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	75	14.4	80.0	454
57	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	76	14.4	80.0	454
58	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	77	14.4	80.0	568
59	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	78	14.4	80.0	568
60	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	79	14.4	80.0	568
61	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	80	14.4	80.0	568
62	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	81	14.4	80.0	568
63	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	82	14.4	80.0	568
64	15.4	85.6	1862	11	US-11-096-5-68A-2408	Sequence 2408, AP	c	83	14.4	80.0	568
65	15.										

C	92	14.4	80.0	584	10	US-10-301-480-682498	Sequence 682498,	165	14	77.8	608	6	US-09-925-065A-862400	Sequence 862400,
C	93	14.4	80.0	588	6	US-09-925-055A-423040	Sequence 423040,	166	14	77.8	613	6	US-09-925-065A-873046	Sequence 873046,
C	94	14.4	80.0	589	6	US-09-925-055A-734243	Sequence 73423,	167	14	77.8	613	6	US-09-925-065A-873047	Sequence 873047,
C	95	14.4	80.0	589	6	US-09-925-055A-734244	Sequence 73424,	168	14	77.8	623	6	US-09-925-065A-867206	Sequence 867206,
C	96	14.4	80.0	589	6	US-09-925-055A-734245	Sequence 73425,	169	14	77.8	623	6	US-09-925-065A-867207	Sequence 867207,
C	97	14.4	80.0	589	9	US-10-301-480-174662	Sequence 174662,	170	14	77.8	640	6	US-09-925-065A-678311	Sequence 678311,
C	98	14.4	80.0	589	9	US-10-301-480-174663	Sequence 174663,	171	14	77.8	640	6	US-09-925-065A-678312	Sequence 678312,
C	99	14.4	80.0	589	9	US-10-301-480-174664	Sequence 174664,	172	14	77.8	680	6	US-09-925-065A-678313	Sequence 678313,
C	100	14.4	80.0	589	10	US-10-301-480-788071	Sequence 788071,	173	14	77.8	777	10	US-10-301-480-598833	Sequence 598833,
C	101	14.4	80.0	589	10	US-10-301-480-788072	Sequence 788072,	174	14	77.8	777	10	US-10-301-480-121242	Sequence 121242,
C	102	14.4	80.0	589	10	US-10-301-480-634503	Sequence 634503,	175	14	77.8	777	10	US-10-301-480-1822-7871	Sequence 7871,
C	103	14.4	80.0	590	6	US-09-925-055A-951767	Sequence 951767,	176	14	77.8	1404	9	US-10-932-182A-79871	Sequence 79871,
C	104	14.4	80.0	593	6	US-09-925-055A-109777	Sequence 109777,	177	14	77.8	1404	9	US-10-932-182A-79871	Sequence 79871,
C	105	14.4	80.0	594	6	US-09-925-055A-819764	Sequence 819764,	178	14	77.8	1588	8	US-10-750-185-25515	Sequence 25515,
C	106	14.4	80.0	594	6	US-09-925-055A-819765	Sequence 819765,	179	14	77.8	1588	8	US-10-750-185-25515	Sequence 25515,
C	107	14.4	80.0	595	6	US-10-301-480-21094	Sequence 21094,	180	14	77.8	2025	6	US-09-925-065A-94759	Sequence 94759,
C	108	14.4	80.0	599	10	US-10-301-480-634503	Sequence 634503,	181	14	77.8	2025	6	US-09-925-065A-94751	Sequence 94751,
C	109	14.4	80.0	600	10	US-10-301-480-518947	Sequence 518947,	182	14	77.8	2025	6	US-09-925-055A-951300	Sequence 951300,
C	110	14.4	80.0	600	10	US-10-301-480-1132356	Sequence 1132356,	183	14	77.8	2025	9	US-10-301-480-196001	Sequence 196001,
C	111	14.4	80.0	601	10	US-10-301-480-33297	Sequence 33297,	184	14	77.8	2025	9	US-10-301-480-196002	Sequence 196002,
C	112	14.4	80.0	601	10	US-10-301-480-33298	Sequence 33298,	185	14	77.8	2025	10	US-10-301-480-809410	Sequence 809410,
C	113	14.4	80.0	601	10	US-10-301-480-946707	Sequence 946707,	186	14	77.8	2025	10	US-10-301-480-809411	Sequence 809411,
C	114	14.4	80.0	601	10	US-10-301-480-946707	Sequence 946707,	187	14	77.8	2025	10	US-10-301-480-809412	Sequence 809412,
C	115	14.4	80.0	606	6	US-09-925-055A-431301	Sequence 431301,	188	14	77.8	2025	10	US-10-301-480-809412	Sequence 809412,
C	116	14.4	80.0	610	6	US-09-925-055A-162218	Sequence 162218,	189	14	77.8	2025	9	US-10-932-182A-177374	Sequence 177374,
C	117	14.4	80.0	610	6	US-10-301-480-71043	Sequence 71043,	190	14	77.8	2025	9	US-10-932-182A-177374	Sequence 177374,
C	118	14.4	80.0	629	9	US-10-301-480-634452	Sequence 634452,	191	14	77.8	2025	9	US-10-932-182A-177374	Sequence 177374,
C	119	14.4	80.0	629	10	US-10-301-480-75387	Sequence 75387,	192	14	77.8	2025	10	US-10-301-480-809411	Sequence 809411,
C	120	14.4	80.0	639	10	US-10-301-480-75387	Sequence 75387,	193	13.8	76.7	18	8	US-10-310-914A-38176	Sequence 8176,
C	121	14.4	80.0	639	10	US-10-301-480-173567	Sequence 173567,	194	13.8	76.7	2025	10	US-10-932-182A-22217	Sequence 22217,
C	122	14.4	80.0	639	10	US-10-301-480-173567	Sequence 173567,	195	13.8	76.7	2025	9	US-10-932-182A-177374	Sequence 177374,
C	123	14.4	80.0	639	10	US-10-301-480-173567	Sequence 173567,	196	13.8	76.7	2025	9	US-10-932-182A-177374	Sequence 177374,
C	124	14.4	80.0	639	10	US-10-301-480-173568	Sequence 173568,	197	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	125	14.4	80.0	639	10	US-10-301-480-173565	Sequence 173565,	198	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	126	14.4	80.0	639	10	US-10-301-480-173566	Sequence 173566,	199	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	127	14.4	80.0	639	10	US-10-301-480-173567	Sequence 173567,	200	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	128	14.4	80.0	639	10	US-10-301-480-173567	Sequence 173567,	201	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	129	14.4	80.0	639	10	US-10-301-480-173567	Sequence 173567,	202	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	130	14.4	80.0	639	10	US-10-301-480-173568	Sequence 173568,	203	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	131	14.4	80.0	639	10	US-10-301-480-173569	Sequence 173569,	204	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	132	14.4	80.0	639	10	US-10-301-480-173570	Sequence 173570,	205	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	133	14.4	80.0	639	10	US-10-301-480-173571	Sequence 173571,	206	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	134	14.4	80.0	639	10	US-10-301-480-173572	Sequence 173572,	207	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	135	14.4	80.0	639	10	US-10-301-480-173573	Sequence 173573,	208	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	136	14.4	80.0	639	10	US-10-301-480-173574	Sequence 173574,	209	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	137	14.4	80.0	639	10	US-10-301-480-173575	Sequence 173575,	210	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	138	14.4	80.0	639	10	US-10-301-480-173576	Sequence 173576,	211	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	139	14.4	80.0	639	10	US-10-301-480-173577	Sequence 173577,	212	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	140	14.4	80.0	639	10	US-10-301-480-173578	Sequence 173578,	213	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	141	14.4	80.0	639	10	US-10-301-480-173579	Sequence 173579,	214	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	142	14.4	80.0	639	10	US-10-301-480-173580	Sequence 173580,	215	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	143	14.4	80.0	639	11	US-11-109-668A-2093	Sequence 2093,	216	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	144	14.4	80.0	639	11	US-11-109-668A-2093	Sequence 2093,	217	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	145	14.4	80.0	639	11	US-10-301-480-173581	Sequence 173581,	218	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	146	14.4	80.0	639	11	US-10-301-480-173582	Sequence 173582,	219	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	147	14.4	80.0	639	11	US-10-301-480-173583	Sequence 173583,	220	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	148	14.4	80.0	639	11	US-10-301-480-173584	Sequence 173584,	221	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	149	14.4	80.0	639	11	US-10-301-480-173585	Sequence 173585,	222	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	150	14.4	80.0	639	11	US-10-301-480-173586	Sequence 173586,	223	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	151	14.4	80.0	639	11	US-10-301-480-173587	Sequence 173587,	224	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	152	14.4	80.0	639	11	US-10-301-480-173588	Sequence 173588,	225	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	153	14.4	80.0	639	11	US-10-301-480-173589	Sequence 173589,	226	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	154	14.4	80.0	639	11	US-10-301-480-173590	Sequence 173590,	227	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	155	14.4	80.0	639	11	US-10-301-480-173591	Sequence 173591,	228	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	156	14.4	80.0	639	11	US-10-301-480-173592	Sequence 173592,	229	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	157	14.4	80.0	639	11	US-10-301-480-173593	Sequence 173593,	230	13.8	76.7	2025	14	US-11-124-368A-18562	Sequence 18562,
C	158	14.4	80.0	639	11	US-10-301-480-173594	Sequence							

ALIGNMENTS

RESULT 1
US-10-301-480-55145
; Sequence 55145, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250, 092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261, 766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289, 846
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 95786
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 504327
 LENGTH: 514
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-504327

Query Match 85.6%; Score 15.4; DB 6; Length 574;
 Best Local Similarity 94.1%; Pred. No. 2.7e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GGACCTAGGGCAAG 18
 Db 361 GGACCCAGGGCAAG 345

RESULT 4

US-09-925-065A-65294/C

; Sequence 65294, Application US/09925065A

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 10827-135
 ; CURRENT APPLICATION NUMBER: US/09/925, 065A

; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243, 096

; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252, 147

; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250, 092

; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261, 766

; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289, 846

; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 65294
 ; LENGTH: 738
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-65294

RESULT 5

US-09-925-065A-65295/C

; Sequence 65295, Application US/09925065A

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827-135
 ; CURRENT APPLICATION NUMBER: US/09/925, 065A

; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/252, 147

; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252, 147

; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/261, 766

; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289, 846

; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 65295
 ; LENGTH: 738
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-65295

RESULT 6

US-09-925-065A-65296/C

; Sequence 65296, Application US/09925065A

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 10827-135
 ; CURRENT APPLICATION NUMBER: US/09/925, 065A

; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243, 096

; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252, 147

; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/261, 766

; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289, 846

; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 65296
 ; LENGTH: 738
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-65296

RESULT 7

US-10-301-480-16653/C

; Sequence 166533, Application US/10301480

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827-135
 ; CURRENT APPLICATION NUMBER: US/09/925, 065A

; CURRENT FILING DATE: 2001-08-08
 ; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 65296
 ; LENGTH: 738
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-65295

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FILE REFERENCE: 108827-137 ; SEQ ID NO 166535
CURRENT APPLICATION NUMBER: US/10/301,480 ; LENGTH: 738
CURRENT FILING DATE: 2002-11-21 ; TYPE: DNA
PRIORITY APPLICATION NUMBER: US 10/215,598 ; ORGANISM: Homo sapien
PRIORITY FILING DATE: 2002-08-09 ; SEQ ID NO 166535
PRIORITY APPLICATION NUMBER: US 60/311,695
PRIORITY FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 166533
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-166533

Query Match 85.6%; Score 15.4; DB 9; Length 738;
Best local Similarity 94.1%; Pred. No. 2.8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACCTAGGGCAAG 18
Db 498 GGACCTAGGAGCAG 482

RESULT 8
US-10-01-480-166534/c
Sequence 166534, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827-137
TITLE OF INVENTION: in the Human Genome
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827-137
CURRENT FILING DATE: 2002-11-21
PRIORITY APPLICATION NUMBER: US 10/215,598
PRIORITY FILING DATE: 2002-08-09
PRIORITY APPLICATION NUMBER: US 60/311,695
PRIORITY FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 166534
LENGTH: 738
TYPE: DNA
PRIORITY APPLICATION NUMBER: US 10/215,598
PRIORITY FILING DATE: 2002-08-09
PRIORITY APPLICATION NUMBER: US 60/311,695
PRIORITY FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 166534
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-166534

Query Match 85.6%; Score 15.4; DB 9; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACCTAGGGCAAG 18
Db 498 GGACCTAGGAGCAG 482

RESULT 10
US-10-301-480-779942/c
Sequence 779942, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827-137
CURRENT FILING DATE: 2002-11-21
PRIORITY APPLICATION NUMBER: US 10/215,598
PRIORITY FILING DATE: 2002-08-09
PRIORITY APPLICATION NUMBER: US 60/311,695
PRIORITY FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 779942
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-779942

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACCTAGGGCAAG 18
Db 498 GGACCTAGGAGCAG 482

RESULT 11
US-10-301-480-779943/c
Sequence 779943, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827-137
CURRENT FILING DATE: 2002-11-21
PRIORITY APPLICATION NUMBER: US 10/215,598
PRIORITY FILING DATE: 2002-08-09
PRIORITY APPLICATION NUMBER: US 60/311,695
PRIORITY FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 779943
LENGTH: 738
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-779943

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2.8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 GGACCCCTAGAGGCAAG 18
Db 498 GGACCCCTAGAGGCAAG 482

RESULT 12
US-10-301-480-779944/c
; Sequence 779944, Application US/10301480
; Publication No. US2006005756A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: In the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 122618
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 779944
; LENGTH: 738
; ORGANISM: Homo sapien
; TYPE: DNA
; US-10-301-480-779944

Query Match 85.6%; Score 15.4; DB 10; Length 738;
Best Local Similarity 94.1%; Pred. No. 2; 8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCCCTAGAGGCAAG 18
Db 498 GGACCCCTAGAGGCAAG 482

RESULT 13
US-10-750-185-61166
; Sequence 61166, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEO_ID NO: 61166
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Bovine 19866881037774
; SEQ ID NO: 61166
; LENGTH: 623-61166

Query Match 85.6%; Score 15.4; DB 8; Length 1155;
Best Local Similarity 94.1%; Pred. No. 2; 8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCCCTAGAGGCAAG 18
Db 869 GGACCCCTAGAGGCAAG 885

RESULT 14
US-10-750-623-61166
; Sequence 61166, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 61166
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Bovine 19866881037774
; SEQ ID NO: 61166
; LENGTH: 623-61166

Query Match 85.6%; Score 15.4; DB 8; Length 1155;
Best Local Similarity 94.1%; Pred. No. 2; 8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGAACCTGAGGCAA 17
Db 1141 CGAACCTGAGGCAA 1125

RESULT 15
US-10-932-182A-2596/c
; Sequence 2596, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, NORIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: FUJIMURA, YUKIKO
; APPLICANT: KODAMA, NORIHIRO
; APPLICANT: ASHIKARI, TOSHIHIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 03085-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS.: 197023
; SOFTWARE: PatentIN version 3.3
; SEQ ID NO: 2596
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; SEQ ID NO: 182A-2596

Query Match 85.6%; Score 15.4; DB 9; Length 1206;
Best Local Similarity 94.1%; Pred. No. 2; 8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGAACCTGAGGCAA 17
Db 1141 CGAACCTGAGGCAA 1125

RESULT 16
US-10-932-182A-2596/c
; Sequence 2596, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, NORIHIRO
; APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO
 APPLICANT: FUJIMURA, TOMOKO
 APPLICANT: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: 030855-043
 CURRENT APPLICATION NUMBER: US/10/932,182A
 CURRENT FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 2596
 LENGTH: 1206
 TYPE: DNA
 ORGANISM: *Saccharomyces pastorianus*

US-10-932-182A-2596

RESULT 17

Query Match 85.6%; Score 15.4; DB 9; Length 1206;
 Best Local Similarity 94.1%; Pred. No. 2.9e-02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGGGCAA 17
 Db 1141 CGGACCTAGGACAAA 1125

US-11-096-568A-33576/C

Sequence 33576, Application US/11096568A
 Publication No. US2006048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A.
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 33576
 LENGTH: 1806
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(1806)
 OTHER INFORMATION: Ceres Seq. ID no. 13603467

US-11-096-568A-33576

Query Match 85.6%; Score 15.4; DB 11; Length 1806;
 Best Local Similarity 94.1%; Pred. No. 3e-02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGCCTAGGCAAG 18
 Db 915 GAGCCCTAGGGCATG 899

RESULT 18

US-11-096-568A-2408/C

Sequence 2408, Application US/11096568A

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Theory
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 2408
 LENGTH: 1862
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 FEATURE:
 NAME/KEY: misc_feature

US-11-096-568A-2408

RESULT 19

Query Match 85.5%; Score 15.4; DB 11; Length 1862;
 Best Local Similarity 94.1%; Pred. No. 3e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTAGGGCAA 18
 Db 948 GGACCTAGGGATG 932

US-11-128-061-856/C

Sequence 856, Application US/11128061
 Publication No. US2006003958A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.
 APPLICANT: Charlebois, Timothy S.
 APPLICANT: Mounts, William M.
 APPLICANT: Hann, Louane E.
 APPLICANT: Sinacore, Martin S.
 APPLICANT: Leonard, Mark W.
 APPLICANT: Brown, Eugene L.
 APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
 FILE REFERENCE: 01997-027701
 CURRENT APPLICATION NUMBER: US/11/128,061
 PRIOR APPLICATION NUMBER: US 60/570,425
 PRIOR FILING DATE: 2004-05-11
 NUMBER OF SEQ ID NOS: 7285
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 856
 LENGTH: 8703
 TYPE: DNA
 ORGANISM: *Mesocricetus auratus*
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (279)..(291)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (331)..(349)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (293)..(321)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (402)..(414)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1384)..(1555)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1728)..(1776)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (2778)..(2795)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature

LOCATION: (3235)..(3257)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (3287)..(3340)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (3342)..(3362)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (4021)..(4025)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (4437)..(4454)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (4895)..(4922)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (7677)..(7701)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (7932)..(7949)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (7861)..(7903)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (7932)..(7949)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (8381)..(8418)
 OTHER INFORMATION: n is a, c, g, or t
 US-11-128-061-856

Query Match 85.6%; Score 15.4; DB 14; Length 8703;
 Best Local Similarity 94.4%; Pred. No. 3.4e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGACCTTAGAGGCAAG 18
 Db 6031 GGACCTTAGAGGCCAG 6015

RESULT 20
 US-11-128-049-856/c
 ; Sequence 856, Application US/11128049
 ; Publication No. US2006010513A1
 GENERAL INFORMATION:
 APPLICANT: Melville, Mark W.
 APPLICANT: Charlebois, Timothy S.
 APPLICANT: Mounts, William M.
 APPLICANT: Hann, Louane E.
 APPLICANT: Sinacore, Martin S.
 APPLICANT: Leonard, Mark W.
 APPLICANT: Brown, Eugene L.
 APPLICANT: Miller, Christopher P.
 TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR CURRENT APPLICATION NUMBER: US/11/128,049
 CURRENT FILING DATE: 2005-05-11
 PRIOR APPLICATION NUMBER: US 60/5570,425
 PRIOR FILING DATE: 2004-05-11
 NUMBER OF SEQ ID NOS: 7285
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 856
 LENGTH: 8703

TYPE: DNA
 ORGANISM: Mesocricetus auratus
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (279)..(291)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (293)..(321)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (331)..(349)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (402)..(414)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (417)..(446)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (4437)..(4454)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (4895)..(4922)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (7677)..(7701)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (7932)..(7949)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (8381)..(8418)

; OTHER INFORMATION: n is a, c, g, or t

US-11-128-049-856

Query Match 85.6%; Score 15.4; DB 14; Length 8703;
Best Local Similarity 94.1%; Pred. No. 3.4e-02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACCTAGGGCAAG 18
Db 6031 GGACCTAGGGCAAG 6015

RESULT 21

US-10-330-773-975/c

; Sequence 975, Application US/10330773
; Publication No. US20060040262A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 52952001300

; CURRENT APPLICATION NUMBER: US/10/330,773

; CURRENT FILING DATE: 2002-12-27

; NUMBER OF SEQ ID NOS: 981

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 975

; LENGTH: 22475

; ORGANISM: Homo sapiens

; FEATURE: misc feature

; LOCATION: (11,-)(22475)

; OTHER INFORMATION: n = A,T,C or G

US-10-330-773-975

Query Match

Best Local Similarity 85.6%; Score 15.4; DB 9; Length 22475;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAGCCCTAGGCGAAAG 18
Db 15390 GGACCTAGGAGAAG 15374

RESULT 22

US-11-124-367A-5024

; Sequence 5024, Application US/11124367A

; GENERAL INFORMATION:

; APPLICANT: Michele Cargill

; APPLICANT: Hongjin Huang

; TITLE OF INVENTION: Genetic Polymorphisms Associated with

; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof

; FILE REFERENCE: CLO01510.ORD

; CURRENT APPLICATION NUMBER: US/11/124,367A

; CURRENT FILING DATE: 2005-05-09

; PRIOR APPLICATION NUMBER: US 60/568,846

; PRIOR FILING DATE: 2004-05-07

; PRIOR APPLICATION NUMBER: US 60/582,609

; PRIOR FILING DATE: 2004-06-25

; PRIOR APPLICATION NUMBER: US 60/599,554

; PRIOR FILING DATE: 2005-08-09

; NUMBER OF SEQ ID NOS: 3460

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5024

; LENGTH: 10000

; TYPE: DNA

; ORGANISM: Homo sapiens
US-11-124-367A-5024

Query Match 85.6%; Score 15.4; DB 14; Length 10000;

; Best Local Similarity 94.1%; Pred. No. 4.1e+02; Mismatches 0; Indels 1; Gaps 0;

; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGGGCAAG 18
Db 27957 GGACCCAGGGCAAG 27973

RESULT 23

US-11-121-086-98/c

; Sequence 98, Application US/11121086

; Publication No. US2005066459A1

; GENERAL INFORMATION:

; APPLICANT: POULSEN, TIM S.

; APPLICANT: NILSEN, KIRSTEN V.

; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

; FILE REFERENCE: 09138_6000-0000

; CURRENT APPLICATION NUMBER: US/11/121,086

; CURRENT FILING DATE: 2005-05-04

; PRIOR APPLICATION NUMBER: 60/567,570

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: Patentin version 3.3

; SEQ ID NO 98

; LENGTH: 171732

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-121-086-98

Query Match 85.6%; Score 15.4; DB 14; Length 171732;

; Best Local Similarity 94.1%; Pred. No. 4.3e+02; Mismatches 1; Indels 0; Gaps 0;

; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGGGCAAG 18
Db 12979 GGACCTAGGGCAAG 12963

RESULT 24

US-11-101-244-1292345

; Sequence 1292346, Application US/11101244

; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; CURRENT APPLICATION NUMBER: US/11/124,367A

; CURRENT FILING DATE: 2005-05-09

; PRIOR APPLICATION NUMBER: US 60/568,846

; PRIOR FILING DATE: 2004-05-07

; PRIOR APPLICATION NUMBER: US 60/582,609

; PRIOR FILING DATE: 2004-06-25

; PRIOR APPLICATION NUMBER: US 60/599,554

; PRIOR FILING DATE: 2005-08-09

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 129346

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-1292346

Query Match 83.3%; Score 15.; DB 12; Length 19;

; Best Local Similarity 93.3%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;

; Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACCTAGGGCAAG 16
Db 4 GGACCUAGGGCAA 18

RESULT 25

US-11-101-244-1292367
; Sequence 1292367, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Diarmacon, Inc.
; APPLICANT: Klyurova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIORITY APPLICATION NUMBER: 60/502,050
; PRIORITY FILING DATE: 2003-09-10
; PRIORITY APPLICATION NUMBER: 60/426,137
; PRIORITY FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1292367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1292367
Query Match 83.3%; Score 15; DB 12; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGACCTTGAGGCAA 16
Db 1 GGACCTTGAGGCAA 15 .

RESULT 26
Sequence 1292346, application US/11083784
Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Diarmacon, Inc.
; APPLICANT: Klyurova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/1083,784
; CURRENT FILING DATE: 2005-03-11
; PRIORITY APPLICATION NUMBER: US/10/714,333
; PRIORITY FILING DATE: 2003-11-14
; PRIORITY APPLICATION NUMBER: 60/502,050
; PRIORITY FILING DATE: 2003-09-10
; PRIORITY APPLICATION NUMBER: 60/426,137
; PRIORITY FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1292367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-1292367
Query Match 83.3%; Score 15; DB 13; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGACCTTGAGGCAA 16
Db 1 GGACCCUGAGGCAA 15 .

RESULT 28
Sequence 965984/c
US-10-310-914A-965984/c
; Sequence 965984, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shili, Kunzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses therefor
; FILE REFERENCE: 06087.0200.CRUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO: 965984
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-965984
Query Match 83.3%; Score 15; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGACCTTGAGGCAA 16
Db 17 GGACCTTGAGGCAA 3 .

RESULT 29
Sequence 1292367, Application US/11083784
US-09-025-065A-99050/c
; Sequence 799050, Application US/09925065A
; Publication No. US200401048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108827.135
 CURRENT APPLICATION NUMBER: US/09/925,065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 PRIOR FILING DATE: 2001-03-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 799050
 LENGTH: 640
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-799050

RESULT 30
 Query Match 83.3%; Score 15; DB 6; Length 640;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GGACCTAGGGCAA 16
 Db 580 GGACCTAGGGCAA 566

RESULT 30
 US-09-925-065A-799051/c
 Sequence 799051, Application US/09925065A
 Publication No. US20040181048A1
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108827.135
 CURRENT APPLICATION NUMBER: US/09/925,065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 799051
 LENGTH: 640
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-799051

Query Match 83.3%; Score 15; DB 6; Length 640;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GGACCTAGGGCAA 16
 Db 580 GGACCTAGGGCAA 566

Search completed: April 15, 2006, 18:19:53
 Job time : 425 secs

Om nucleic - nucleic search, using sw model

Run on: April 15, 2006, 18:09:33 ; Search time 806 Seconds
 (without alignments)
 18.4.676 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18

Sequence: 1 cggacccataggcgaag 18

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 9793542 seqs, .4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications_NA_Main.*

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2: /cgn2_6/ptodata/1/pubpna/us08_pubcomb.seq:*

3: /cgn2_6/ptodata/1/pubpna/us09A_pubcomb.seq:*

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9: /cgn2_6/ptodata/1/pubpna/us11_pubcomb.seq:*

10: /cgn2_6/ptodata/1/pubpna/us11_pubcomb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	18	100.0	18	8 US-10-727-358-5
2	18	100.0	18	8 US-10-727-358-15
3	18	100.0	18	8 US-10-727-358-28
4	18	100.0	25	10 US-11-036-317-90438
5	18	100.0	25	10 US-11-036-317-90438
6	18	100.0	25	10 US-11-036-317-90438
7	18	100.0	120	8 US-10-727-358-1
8	18	100.0	121	8 US-10-727-358-25
9	18	100.0	2601	8 US-10-727-358-24
10	18	100.0	2622	6 US-10-085-117-33
11	18	100.0	4094	6 US-10-085-117-32
12	18	100.0	4094	8 US-10-727-358-11
13	16.4	91.1	25	10 US-11-036-317-881395
14	16.4	91.1	25	10 US-11-036-317-904637
15	16.4	91.1	25	10 US-11-036-317-910915
16	16.8	88.9	16	8 US-10-727-358-8
17	16	88.9	25	10 US-11-036-317-928166
18	15.4	85.6	233	7 US-10-242-532A-12278
19	15.4	85.6	233	7 US-10-027-632A-12278
20	15.4	85.6	376	3 US-09-964-828A-522
21	15.4	85.6	376	3 US-09-965-828A-522
22	15.4	85.6	376	9 US-10-843-641A-5825
23	15.4	85.6	376	9 US-10-843-641A-7538

24 15.4 85.6 383 8 US-10-425-115-110504 Sequence 110504,
 25 15.4 85.6 481 5 US-10-027-632-141547 Sequence 141547,
 26 15.4 85.6 481 6 US-10-027-632-141547 Sequence 141547,
 27 15.4 85.6 514 3 US-10-974-872-162 Sequence 162, APP
 28 15.4 85.6 546 5 US-10-027-632-20268 Sequence 20268,
 29 15.4 85.6 546 7 US-10-027-632-20268 Sequence 52757, A
 30 15.4 85.6 547 7 US-10-424-593-52757 Sequence 504327,
 31 15.4 85.6 574 4 US-09-925-055A-65296 Sequence 228051,
 32 15.4 85.6 611 5 US-10-027-632-228051 Sequence 65294, A
 33 15.4 85.6 611 6 US-10-027-632-228051 Sequence 65295, A
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 35 15.4 85.6 738 4 US-09-925-055A-65295 Sequence 65296, A
 36 15.4 85.6 738 4 US-10-424-593-52757 Sequence 65296, A
 37 15.4 85.6 751 5 US-10-027-632-19033 Sequence 19033, A
 38 15.4 85.6 751 5 US-10-027-632-19033 Sequence 19033, A
 39 15.4 85.6 1797 8 US-10-723-860-895 Sequence 7641, APP
 40 15.4 85.6 9645 9 US-10-723-860-895 Sequence 895, APP
 41 15.4 85.6 9645 9 US-10-756-119-895 Sequence 895, APP
 42 15.4 85.6 314364 9 US-10-917-647-3 Sequence 3, APP
 43 15.4 83.3 50 6 US-10-131-837-7589 Sequence 7589, APP
 44 15.4 83.3 75 8 US-10-166-884-1319 Sequence 1339, APP
 45 15.4 83.3 265 7 US-10-085-703A-13707 Sequence 13707, APP
 46 15.4 83.3 285 7 US-10-424-559-13075 Sequence 139075, APP
 47 15.4 83.3 306 7 US-10-424-559-34328 Sequence 34328, APP
 48 15.4 83.3 320 7 US-10-244-535A-6362 Sequence 6362, APP
 49 15.4 83.3 320 7 US-10-085-703A-6362 Sequence 6362, APP
 50 15.4 83.3 327 7 US-10-242-535A-13737 Sequence 13737, APP
 51 15.4 83.3 327 7 US-10-085-703A-13737 Sequence 13737, APP
 52 15.4 83.3 327 7 US-10-085-703A-13737 Sequence 13737, APP
 53 15.4 83.3 342 3 US-09-978-178-1956 Sequence 1996, APP
 54 15.4 83.3 342 5 US-10-146-502-1956 Sequence 1996, APP
 55 15.4 83.3 412 3 US-09-918-905-37155 Sequence 37155, APP
 56 15.4 83.3 412 3 US-09-918-905-37155 Sequence 37155, APP
 57 15.4 83.3 444 3 US-09-822-846-548 Sequence 548, APP
 58 15.4 83.3 478 3 US-09-918-905-15549 Sequence 16549, APP
 59 15.4 83.3 554 3 US-09-764-869-334 Sequence 334, APP
 60 15.4 83.3 554 3 US-10-091-004-334 Sequence 334, APP
 61 15.4 83.3 554 6 US-10-227-577-334 Sequence 334, APP
 62 15.4 83.3 576 5 US-10-027-632-282238 Sequence 282238,
 63 15.4 83.3 576 6 US-10-027-632-282238 Sequence 282238,
 64 15.4 83.3 600 9 US-10-956-157-7765 Sequence 7765, APP
 65 15.4 83.3 606 5 US-10-027-632-60295 Sequence 60295, APP
 66 15.4 83.3 606 5 US-10-027-632-60295 Sequence 60295, APP
 67 15.4 83.3 606 6 US-10-027-632-60295 Sequence 60295, APP
 68 15.4 83.3 606 6 US-10-027-632-305560 Sequence 305560,
 69 15.4 83.3 627 3 US-09-971-192-213 Sequence 213, APP
 70 15.4 83.3 640 4 US-09-925-065A-799050 Sequence 799050,
 71 15.4 83.3 640 4 US-09-925-065A-799051 Sequence 799051,
 72 15.4 83.3 640 4 US-09-925-065A-799052 Sequence 799052,
 73 15.4 83.3 669 4 US-09-925-065A-799053 Sequence 799053,
 74 15.4 83.3 669 4 US-09-925-065A-853128 Sequence 853128,
 75 15.4 83.3 679 4 US-10-956-157-2330 Sequence 2530, APP
 76 15.4 83.3 779 3 US-09-882-846-549 Sequence 549, APP
 77 15.4 83.3 782 3 US-09-890-688-95 Sequence 95, APP
 78 15.4 83.3 782 6 US-10-087-192-280 Sequence 95, APP
 79 15.4 83.3 782 6 US-10-087-192-280 Sequence 95, APP
 80 15.4 83.3 5760 10 US-11-097-143-2785 Sequence 23785, APP
 81 15.4 83.3 47479 5 US-10-087-192-280 Sequence 23785, APP
 82 15.4 83.3 47479 5 US-10-087-192-280 Sequence 23785, APP
 83 15.4 83.3 122937 7 US-10-322-281-694 Sequence 694, APP
 84 15.4 83.3 421609 7 US-10-367-994-122 Sequence 122, APP
 85 15.4 83.3 3299 9 US-10-915-740-638 Sequence 638, APP
 86 15.4 83.3 486 8 US-10-425-115-29192 Sequence 129192,
 87 15.4 83.3 529 8 US-10-425-115-7702 Sequence 75029, APP
 88 15.4 83.3 566 4 US-09-925-065A-585895 Sequence 758596,
 89 15.4 83.3 566 4 US-09-925-065A-585895 Sequence 25209, APP
 90 15.4 83.3 588 4 US-09-925-065A-585895 Sequence 585830,
 91 15.4 83.3 588 4 US-09-925-065A-585895 Sequence 585831,
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 95 15.4 83.3 588 4 US-09-925-065A-585895 Sequence 585835,
 96 15.4 83.3 588 4 US-09-925-065A-585895 Sequence 585836,

C	97	14.8	82.2	1115	7	US-10-425-114-34866	Sequence 34866, A	C	170	14.4	80.0	606	4	US-09-925-05A-431301
C	98	14.8	82.2	1706	8	US-10-425-115-141838	Sequence 141838, A	C	171	14.4	80.0	610	4	Sequence 462218,
C	99	14.8	82.2	2005	8	US-10-767-795-3352	Sequence 3352, A	C	172	14.4	80.0	5	US-10-027-632-224705	
C	100	14.8	82.2	2044	3	US-10-822-849A-3119	Sequence 3119, A	C	173	14.4	80.0	610	5	Sequence 224705,
C	101	14.8	82.2	2339	6	US-10-264-237-2839	Sequence 2839, A	C	174	14.4	80.0	610	5	Sequence 224707,
C	102	14.8	82.2	2870	10	US-10-971-143-20968	Sequence 20968, A	C	175	14.4	80.0	610	6	Sequence 224705,
C	103	14.8	82.2	2981	6	US-10-264-237-2840	Sequence 2840, A	C	176	14.4	80.0	610	6	Sequence 224706,
C	104	14.8	82.2	3006	10	US-11-097-143-21799	Sequence 21799, A	C	177	14.4	80.0	610	5	Sequence 224707,
C	105	14.8	82.2	3469	7	US-10-603-725-23	Sequence 23, A	C	178	14.4	80.0	616	5	Sequence 93222, A
C	106	14.8	82.2	3511	7	US-10-603-725-19	Sequence 19, A	C	179	14.4	80.0	616	5	Sequence 307702,
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C	114	14.8	82.2	3971	3	US-09-876-176-1	Sequence 17, A	C	187	14.4	80.0	636	8	Sequence 307702,
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C	116	14.8	82.2	3971	6	US-10-295-027-319	Sequence 319, A	C	189	14.4	80.0	658	8	Sequence 275520,
C	117	14.8	82.2	3971	7	US-10-390-060-1	Sequence 25, A	C	190	14.4	80.0	663	5	Sequence 275521,
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C	130	14.8	82.2	55611	6	US-10-017-161-783	Sequence 783, A	C	203	14.4	80.0	813	4	Sequence 25469, A
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C	142	14.4	80.0	380	8	US-10-767-795-2267	Sequence 2267, A	C	215	14.4	80.0	1334	4	Sequence 25471, A
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C	145	14.4	80.0	475	3	US-09-764-878-18	Sequence 18, A	C	218	14.4	80.0	2621	10	US-11-097-143-36334
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C	147	14.4	80.0	479	3	US-09-962-436-171	Sequence 171, A	C	220	14.4	80.0	2754	3	Sequence 172393, A
C	148	14.4	80.0	479	9	US-10-843-641A-2630	Sequence 2630, A	C	221	14.4	80.0	3153	6	Sequence 66972, A
C	149	14.4	80.0	542	5	US-10-273-632-284801	Sequence 284801, A	C	222	14.4	80.0	7036	7	Sequence 124611, A
C	150	14.4	80.0	542	6	US-10-027-632-284801	Sequence 284801, A	C	223	14.4	80.0	8133	3	Sequence 157312, A
C	151	14.4	80.0	564	5	US-10-433-579-14	Sequence 14, A	C	224	14.4	80.0	1262	4	Sequence 173313, A
C	152	14.4	80.0	564	5	US-10-178-782-1	Sequence 1, A	C	225	14.4	80.0	1262	4	Sequence 173313, A
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C	155	14.4	80.0	579	4	US-09-925-065A-625667	Sequence 625667, A	C	228	14.4	80.0	17953	5	Sequence 173313, A
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C	157	14.4	80.0	581	6	US-10-074-778A-19	Sequence 19, A	C	230	14.4	80.0	17953	5	Sequence 173313, A
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C	161	14.4	80.0	589	4	US-09-925-065A-734243	Sequence 734243, A	C	234	14.4	80.0	17953	5	Sequence 173313, A
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C	164	14.4	80.0	590	4	US-09-925-065A-734243	Sequence 734243, A	C	237	14.4	80.0	17953	5	Sequence 173313, A
C	165	14.4	80.0	592	6	US-10-029-386-701	Sequence 7011, A	C	238	14.4	80.0	17953	5	Sequence 173313, A
C	166	14.4	80.0	593	4	US-09-925-065A-109777	Sequence 109777, A	C	239	14.4	80.0	17953	5	Sequence 173313, A
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C	168	14.4	80.0	594	4	US-09-925-065A-81766	Sequence 81766, A	C	241	14.4	80.0	17953	5	Sequence 173313, A
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RESULT 1
US-10-727-358-5
; Sequence 5, Application US/10727358
; Publication No. US2005037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS

C	243	14	77.8	201	8	US-10-719-993-47907	Sequence 47907, A
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C	246	14	77.8	201	8	US-10-741-600-39100	Sequence 39100, A
C	247	14	77.8	201	8	US-10-741-600-42189	Sequence 42189, A
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C	249	14	77.8	201	8	US-10-741-600-63954	Sequence 63954, A
C	250	14	77.8	342	8	US-10-425-115-62875	Sequence 62875, A
C	251	14	77.8	515	4	US-03-925-065A-131156	Sequence 131156, A
C	252	14	77.8	516	4	US-03-925-065A-193359	Sequence 193359, A
C	253	14	77.8	552	4	US-03-925-065A-523294	Sequence 523294, A
C	254	14	77.8	557	4	US-03-925-065A-727874	Sequence 727874, A
C	255	14	77.8	564	4	US-03-925-065A-730746	Sequence 730746, A
C	256	14	77.8	580	4	US-03-925-065A-921733	Sequence 921733, A
C	257	14	77.8	585	3	US-03-917-804-884	Sequence 884, A
C	258	14	77.8	607	6	US-10-027-632-216677	Sequence 216677, A
C	259	14	77.8	607	6	US-10-027-632-216677	Sequence 216677, A
C	260	14	77.8	608	4	US-03-925-065A-862399	Sequence 862399, A
C	261	14	77.8	608	4	US-03-925-065A-862400	Sequence 862400, A
C	262	14	77.8	613	4	US-03-925-065A-873046	Sequence 873046, A
C	263	14	77.8	613	4	US-03-925-065A-8731047	Sequence 8731047, A
C	264	14	77.8	616	8	US-10-653-047-2321	Sequence 2321, A
C	265	14	77.8	623	4	US-03-925-065A-867206	Sequence 867206, A
C	266	14	77.8	623	4	US-03-925-065A-867207	Sequence 867207, A
C	267	14	77.8	640	4	US-03-925-065A-678312	Sequence 678312, A
C	268	14	77.8	640	4	US-03-925-065A-678313	Sequence 678313, A
C	269	14	77.8	644	6	US-10-027-632-285597	Sequence 285597, A
C	270	14	77.8	644	6	US-10-027-632-285597	Sequence 285597, A
C	271	14	77.8	644	6	US-10-027-632-285597	Sequence 285597, A
C	272	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
C	273	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
C	274	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
C	275	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
C	276	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
C	277	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
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C	289	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
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C	296	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
C	297	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
C	298	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A
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C	300	14	77.8	644	6	US-03-925-065A-709785	Sequence 709785, A

ALIGNMENTS

RESULT 2
US-10-727-358-5
; Sequence 15, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS

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Db	1	GGGACCTAGGCAAG	18

RESULT 3
US-10-727-358-5.rnpbm
; Sequence 28, Application US/10727358
; Publication No. US20050037455A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED

Ov	1	GGGACCTAGGCAAG	18
Db	1	GGGACCTAGGCAAG	18

Query 1 CGGACCTAGGCAAG 18
Database 1 OGGACCTAGGCAAG 18

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/450,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense oligonucleotide
; US-10-727-358-28

Query Match 100.0%; Score 18; DB 8; Length 18;
; Best Local Similarity 100.0%; Pred. No. 28;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 CGGACCTAGAGGAAG 18
; Db 18 CGGACCTAGAGGAAG 1

RESULT 4

Query Match 100.0%; Score 18; DB 8; Length 18;
; Best Local Similarity 100.0%; Pred. No. 28;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 CGGACCTAGAGGAAG 18
; Db 18 CGGACCTAGAGGAAG 1

RESULT 6

Query Match 100.0%; Score 18; DB 10; Length 25;
; Best Local Similarity 100.0%; Pred. No. 27;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 CGGACCTAGAGGAAG 18
; Db 2 CGGACCTAGAGGAAG 19

RESULT 5

Query Match 100.0%; Score 18; DB 10; Length 25;
; Best Local Similarity 100.0%; Pred. No. 27;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 CGGACCTAGAGGAAG 18
; Db 4 CGGACCTAGAGGAAG 21

; ORGANISM: Mus musculus
; US-11-036-317-881396

Query Match 100.0%; Score 18; DB 10; Length 25;
; Best Local Similarity 100.0%; Pred. No. 27;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654-1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 99174
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO: 881396
; LENGTH: 25
; TYPE: DNA

RESULT 4

Query Match 100.0%; Score 18; DB 10; Length 25;
; Best Local Similarity 100.0%; Pred. No. 27;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 CGGACCTAGAGGAAG 18
; Db 18 CGGACCTAGAGGAAG 1

RESULT 6

Query Match 100.0%; Score 18; DB 10; Length 25;
; Best Local Similarity 100.0%; Pred. No. 27;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 CGGACCTAGAGGAAG 18
; Db 2 CGGACCTAGAGGAAG 19

RESULT 7

Query Match 100.0%; Score 18; DB 10; Length 25;
; Best Local Similarity 100.0%; Pred. No. 27;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Xing, Hong-Mei R.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATE
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/450,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-727-358-1

Query Match 100.0%; Score 18; DB 8; Length 120;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CGGACCTAGGGCAAG 18
 Db 91 CGGACCTAGGGCAAG 108

RESULT 8

US-10-727-358-25

Sequence 25, Application US/10727358

Publication No. US20050037455A1

GENERAL INFORMATION:

APPLICANT: Memorial Sloan-Kettering Cancer Center

APPLICANT: Kolesnick, Richard N.

APPLICANT: Xing, Hong-Mei R.

TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED

FILE REFERENCE: 1216-1-006CIP

CURRENT APPLICATION NUMBER: US/10/727,358

CURRENT FILING DATE: 2003-12-03

PRIOR APPLICATION NUMBER: 60/384,228

PRIOR FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: 60/460,023

PRIOR FILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: PCT/US03/16961

PRIOR FILING DATE: 2003-05-29

NUMBER OF SEQ ID NOS: 38

SEQ ID NO: 25

LENGTH: 121

TYPE: DNA

ORGANISM: Homo sapiens

US-10-727-358-25

Query Match 100.0%; Score 18; DB 8; Length 121;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 18; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

RESULT 9

US-10-727-358-24

Sequence 24, Application US/10727358

Publication No. US20050037455A1

GENERAL INFORMATION:

APPLICANT: Memorial Sloan-Kettering Cancer Center

APPLICANT: Kolesnick, Richard N.

APPLICANT: Xing, Hong-Mei R.

TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED

FILE REFERENCE: 1216-1-006CIP

CURRENT APPLICATION NUMBER: US/10/727,358

CURRENT FILING DATE: 2003-12-03

PRIOR APPLICATION NUMBER: PCT/US03/16961

PRIOR FILING DATE: 2003-05-29

NUMBER OF SEQ ID NOS: 38

SEQ ID NO: 24

LENGTH: 2601

TYPE: DNA

ORGANISM: Homo sapiens

US-10-727-358-24

Query Match 100.0%; Score 18; DB 8; Length 2601;

Query Match

Best Local Similarity 100.0%; Pred. No. 15;
 Matches 18; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CGGACCTAGGGCAAG 18
 Db 187 CGGACCCTAGGGCAAG 204

RESULT 10

US-10-085-117-33

Sequence 33, Application US/10085117

Publication No. US20030232334A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhardt, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REFERENCE: 529452000121

CURRENT APPLICATION NUMBER: US/10/085,117

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 33

LENGTH: 2622

TYPE: DNA

ORGANISM: Mus musculus

US-10-085-117-33

Query Match 100.0%; Score 18; DB 6; Length 4094;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 18; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

RESULT 11

US-10-085-117-32

Sequence 32, Application US/10085117

Publication No. US20030232334A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhardt, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REFERENCE: 529452000121

CURRENT APPLICATION NUMBER: US/10/085,117

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 32

LENGTH: 4094

TYPE: DNA

ORGANISM: Mus musculus

US-10-085-117-32

Query Match 100.0%; Score 18; DB 6; Length 4094;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 18; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

RESULT 12

US-10-727-358-11

Sequence 11, Application US/10727358

Publication No. US20050037455A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhardt, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REFERENCE: 529452000121

CURRENT APPLICATION NUMBER: US/10/085,117

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 32

LENGTH: 4094

TYPE: DNA

ORGANISM: Mus musculus

US-10-085-117-32

APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 11
; LENGTH: 4094
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-727-358-11

Query Match 100.0%; Score 18; DB 8; Length 4094;
Best local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGCCAAG 18
Db 296 CGGACCTAGAGCCAAG 313

RESULT 13
US-11-036-317-881395
; Sequence 881395, Application US/11036317
; Publication No. US2005021423A1

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO: 881395
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-881395

Query Match 91.1%; Score 16.4; DB 10; Length 25;
Best local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGCCAAG 18
Db 4 CGGACCTAGAGCCAAG 21

RESULT 14
US-11-036-317-904637
; Sequence 904637, Application US/11036317
; Publication No. US2005021482A1

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence

RESULT 15
US-11-036-317-910915
; Sequence 910915, Application US/11036317
; Publication No. US2005021482A1

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO: 910915
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-910915

Query Match 91.1%; Score 16.4; DB 10; Length 25;
Best local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGACCTAGAGCCAAG 18
Db 1 CGGACCTAGAGCCAAG 18

RESULT 16
US-10-727-358-8/C
; Sequence 8, Application US/10727358
; Publication No. US20050037455A1

; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; APPLICANT: Kolesnick, Richard N.
; TITLE OF INVENTION: KINASE SUPPRESSOR OF RAS INACTIVATION FOR THERAPY OF RAS MEDIATED
; TITLE OF INVENTION: TUMORIGENESIS
; FILE REFERENCE: 1216-1-006CIP
; CURRENT APPLICATION NUMBER: US/10/727,358
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/384,228
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/460,023
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: PCT/US03/16961
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: antisense oligonucleotide
; US-10-727-358-8

Query Match 88.9%; Score 16; DB 8; Length 16;
; Best Local Similarity 100.0%; Pred. No. 3.1e+02;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACCTAGAGGCAAG 18
Db ||||| ||||| |||||
16 GACCTAGAGGCAAG 1

RESULT 17
US-11-036-317-928166

Sequence 928166, Application US/11036317
; Publication No. US20050214823A1

; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; LENGTH: 25
; SEQ ID NO 928166
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-928166

RESULT 18
Query Match 88.9%; Score 16; DB 10; Length 25;
; Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACCTAGAGGCAAG 18
Db ||||| ||||| |||||
1 GACCTAGAGGCAAG 16

RESULT 19
US-10-085-783A-12378/C

Sequence 12378, Application US/10085783A
; Publication No. US20040037841A1

; GENERAL INFORMATION:
; APPLICANT: Chondrogenic Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/3105,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12378
; LENGTH: 233
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)..(28)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)..(28)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)..(28)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (66)..(66)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-085-783A-12378

Query Match 85.6%; Score 15.4; DB 7; Length 233;
; Best Local Similarity 94.1%; Pred. No. 4.6e+02;
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 20
 Qy 2 GGACCTCTAGGCGAAG 18
 Db 188 GGACCTCTAGGCGCAG 172

GENERAL INFORMATION:
 APPLICANT: Horrigan, Stephen
 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

RESULT 22
 US-09-964-824A-522/c
 Sequence 5825, Application US/10843641A
 Publication No. US/00500644541A

GENERAL INFORMATION:
 APPLICANT: Avalon Pharmaceuticals, Inc.
 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

FILE REFERENCE: 689290-189
 CURRENT APPLICATION NUMBER: US/10/843,641A
 CURRENT FILING DATE: 2001-09-27
 PRIOR APPLICATION NUMBER: US/09/873,367
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US/09/954,531
 PRIOR FILING DATE: 2001-09-18
 PRIOR APPLICATION NUMBER: US/09/954,456
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/962,436
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/962,832
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/964,824
 PRIOR FILING DATE: 2001-09-27
 PRIOR APPLICATION NUMBER: US/09/967,768
 PRIOR FILING DATE: 2001-09-28
 PRIOR APPLICATION NUMBER: US/09/968,007
 PRIOR FILING DATE: 2001-10-02
 PRIOR APPLICATION NUMBER: US/09/969,347
 PRIOR FILING DATE: 2001-10-02
 PRIOR APPLICATION NUMBER: US/09/969,708
 PRIOR FILING DATE: 2001-10-03
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 8447

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5825
 LENGTH: 376
 TYPE: DNA
 ORGANISM: Homo sapiens

US-09-964-824A-522

RESULT 21
 Query Match Best Local Similarity 94.1%; Pred. No. 4.4e+02; Length 376;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: Augustus, Meena
 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

FILE REFERENCE: 689290-70
 CURRENT APPLICATION NUMBER: US/09/969,708
 CURRENT FILING DATE: 2001-10-03
 PRIOR APPLICATION NUMBER: US/60/237,606
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: US/60/237,608
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: US/60/237,425
 PRIOR FILING DATE: 2000-10-03
 NUMBER OF SEQ ID NOS: 658
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 67
 LENGTH: 376
 TYPE: DNA
 ORGANISM: Homo sapiens

US-09-963-708-67

RESULT 22
 US-09-963-708-67/c
 Sequence 5825, Application US/10843641A
 Publication No. US/00500644541A

GENERAL INFORMATION:
 APPLICANT: Avalon Pharmaceuticals, Inc.
 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

FILE REFERENCE: 689290-189
 CURRENT APPLICATION NUMBER: US/10/843,641A
 CURRENT FILING DATE: 2004-05-12
 PRIOR APPLICATION NUMBER: US/09/873,367
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US/09/954,531
 PRIOR FILING DATE: 2001-09-18
 PRIOR APPLICATION NUMBER: US/09/954,456
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/962,436
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/962,832
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/964,824
 PRIOR FILING DATE: 2001-09-27
 PRIOR APPLICATION NUMBER: US/09/967,768
 PRIOR FILING DATE: 2001-09-28
 PRIOR APPLICATION NUMBER: US/09/968,007
 PRIOR FILING DATE: 2001-10-02
 PRIOR APPLICATION NUMBER: US/09/969,347
 PRIOR FILING DATE: 2001-10-02
 PRIOR APPLICATION NUMBER: US/09/969,708
 PRIOR FILING DATE: 2001-10-03
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 8447

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5825
 LENGTH: 376
 TYPE: DNA
 ORGANISM: Homo sapiens

US-10-843-641A-5825

RESULT 23
 US-10-843-641A-753B/c
 Sequence 7538, Application US/10843641A
 Publication No. US/00500644541A

GENERAL INFORMATION:
 APPLICANT: Avalon Pharmaceuticals, Inc.
 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

FILE REFERENCE: 689290-189
 CURRENT APPLICATION NUMBER: US/10/843,641A
 CURRENT FILING DATE: 2004-05-12
 PRIOR APPLICATION NUMBER: US/09/873,367
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US/09/954,531
 PRIOR FILING DATE: 2001-09-18
 PRIOR APPLICATION NUMBER: US/09/954,456
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/962,436
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/962,832
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09/964,824

Query Match Best Local Similarity 94.1%; Pred. No. 4.4e+02; Length 376;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: DNA
 TITLE OF INVENTION: Organism: Homo sapiens

TYPE: DNA
 ORGANISM: Homo sapiens

US-09-963-708-67

Query Match Best Local Similarity 94.1%; Pred. No. 4.4e+02; Length 376;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: DNA
 TITLE OF INVENTION: Organism: Homo sapiens

TYPE: DNA
 ORGANISM: Homo sapiens

US-09-963-708-67

```

; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 847
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 7538
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-843-641A-7538

RESULT 24
Query Match      85.6%; Score 15.4; DB 9; Length 376;
Best Local Similarity 94.1%; Pred. No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy   2 GGACCTAGGGCAAG 18
Db   107 ||GACCTAGGGCAAG 91

RESULT 24
US-10-425-115-110504
Sequence 110504, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 110504
LENGTH: 383
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_32272C.1
US-10-425-115-110504

Query Match      85.6%; Score 15.4; DB 8; Length 383;
Best Local Similarity 94.1%; Pred. No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy   2 GGACCTAGGGCAAG 18
Db   3 GACCTCGAGGCAAG 19

RESULT 25
US-10-027-632-141547
Sequence 141547, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827-129
CURRENT FILING NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 141547
LENGTH: 481
TYPE: DNA
ORGANISM: Human
US-10-027-632-141547

Query Match      85.6%; Score 15.4; DB 6; Length 481;
Best Local Similarity 94.1%; Pred. No. 4.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy   2 GGACCTAGGGCAAG 18
Db   255 GACCCAGGGCAAG 271

RESULT 26
US-10-027-632-141547
Sequence 141547, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827-129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 141547
LENGTH: 481
TYPE: DNA
ORGANISM: Human
US-10-027-632-141547

Query Match      85.6%; Score 15.4; DB 6; Length 481;
Best Local Similarity 94.1%; Pred. No. 4.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy   2 GGACCTAGGGCAAG 18
Db   255 GACCCAGGGCAAG 271

RESULT 27
US-09-764-872-163/C
Sequence 162, Application US/09764872

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Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-872-162

Query Match Best Local Similarity 94.1%; Score 15.4; DB 3; Length 514; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGGCAAG 18
Db 430 GGACCTAGGCAAG 414

RESULT 28
US-10-027-632-202268
; Publication 202268, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 202268
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-202268

Query Match Best Local Similarity 94.1%; Score 15.4; DB 6; Length 546; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGGCAAG 18
Db 62 GGACCTAGGCAAG 78

RESULT 30
US-10-24-599-52757
; Sequence 52757, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 52757
; LENGTH: 547
; TYPE: DNA
; FEATURE: Glycine max
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18652C.1
; US-10-424-599-52757

Query Match Best Local Similarity 94.1%; Score 15.4; DB 5; Length 546; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGGCAAG 18
Db 62 GGACCTAGGCAAG 78

RESULT 29
US-10-027-632-202268

; Sequence 202268, Application US/10027632

; Publication No. US200302204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

Search completed: April 16, 2006, 01:39:37
Job time : 8.9 sec

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GenFore version 5.1.7

OM nucleic - nucleic search, using sw model
Run on: April 15, 2006, 17:47:14 ; Search time 3806 Seconds
(without alignments)
221.274 Million cell updates/sec

Title: US-10-727-358-5

Perfect score: 18

Sequence: 1 cggaccctaggccaag 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

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EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gbs1:*
10: gb_gbs2:*
11: gb_gbs3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	18	100.0	656	2 BB629501	BB629501 BB629501
2	18	100.0	674	5 BY727643	BY727643 BY727643
3	18	100.0	688	2 BB613725	BB613725 BB613725
4	18	100.0	2751	4 AK035565	AK035565 Mus muscu
5	16.4	91.1	317	7 CK370327	CK370327 zmrww005
6	16.4	91.1	370	4 CF633652	CF633652 zmrww007
7	16.4	91.1	510	2 BE171998	BE171998 PML-HTO79
8	16.4	91.1	704	10 AG334283	AG334283 Mus muscu
9	16.4	91.1	744	8 DP059598	DP059598 AGENCOURT
10	16.4	91.1	817	8 CX910994	CX910994 JGG1_CNA2
11	16.4	91.1	875	8 DT058819	DT058819 AGENCOURT
12	16	88.9	296	8 BB247762	BB247762 BB247762
13	16	88.9	396	2 BE768604	BE768604 QV2-FP001
14	16	88.9	430	1 AI762325	AI762325 wq97404.x
15	16	88.9	507	1 BM029828	BM029828 488200 MA
16	16	88.9	538	1 AI208178	AI208178 q955abw.x
17	16	88.9	769	10 AG498153	AG498153 Mus muscu
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20	15.4	85.6	170	1 AA654607	AA654607 nt59802.8
21	15.4	85.6	177	1 AA234751	AA234751 z83805.8
22	15.4	85.6	205	1 AI099443	AI099443 ue30f06.X

C	96	15.4	85.6	572	10	CB785184	C	169	15	83.3	175	1	AA151954
C	97	15.4	85.6	573	9	B2539545	C	170	15	83.3	179	1	AA595944
C	98	15.4	85.6	574	7	CK90522	C	171	15	83.3	180	2	B1005692
C	99	15.4	85.6	577	9	AZ59114	C	172	15	83.3	182	1	AA481544
C	100	15.4	85.6	579	9	B2539539	C	173	15	83.3	185	5	BU670987
C	101	15.4	85.6	579	11	CR116258	C	174	15	83.3	193	1	AA853831
C	102	15.4	85.6	580	5	BW148814	C	175	15	83.3	194	2	BB035839
C	103	15.4	85.6	596	9	AQ918955	C	176	15	83.3	201	1	AA720956
C	104	15.4	85.6	606	3	BM013427	C	177	15	83.3	206	1	AA33183
C	105	15.4	85.6	611	5	BQ77182	C	178	15	83.3	209	1	BB311723
C	106	15.4	85.6	612	7	CK905521	C	179	15	83.3	213	1	AA134926
C	107	15.4	85.6	621	2	BB656765	C	180	15	83.3	215	1	AW103581
C	108	15.4	85.6	621	6	CDT05000	C	181	15	83.3	217	1	CM260725
C	109	15.4	85.6	635	3	BM831637	C	182	15	83.3	225	1	AI825290
C	110	15.4	85.6	636	5	BX417723	C	183	15	83.3	226	1	AA459415
C	111	15.4	85.6	640	8	CX182808	C	184	15	83.3	228	2	BE018221
C	112	15.4	85.6	642	7	CK05791	C	185	15	83.3	228	2	CK157899
C	113	15.4	85.6	649	7	CK757899	C	186	15	83.3	230	1	AL654782
C	114	15.4	85.6	653	10	CE755366	C	187	15	83.3	233	1	AB186432
C	115	15.4	85.6	664	9	BZ144550	C	188	15	83.3	239	2	BI021689
C	116	15.4	85.6	669	2	BF965563	C	189	15	83.3	243	1	AA506757
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C	118	15.4	85.6	685	10	AG1517422	C	191	15	83.3	250	1	AK352063
C	119	15.4	85.6	686	8	DN151938	C	192	15	83.3	251	1	AB370233
C	120	15.4	85.6	696	5	BI61828	C	193	15	83.3	253	1	AA961889
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C	122	15.4	85.6	725	10	AG438387	C	195	15	83.3	257	1	AW174594
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C	124	15.4	85.6	788	5	BUS32673	C	197	15	83.3	257	8	CA477221
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C	126	15.4	85.6	792	11	CR103388	C	199	15	83.3	265	1	AA19779
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C	128	15.4	85.6	813	5	BUS37587	C	201	15	83.3	274	2	BI21698
C	129	15.4	85.6	813	9	BIH107451	C	202	15	83.3	275	1	AW1878821
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C	132	15.4	85.6	845	6	BX244346	C	205	15	83.3	283	2	AB105934
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C	135	15.4	85.6	858	9	BZ339723	C	208	15	83.3	292	1	AI673126
C	136	15.4	85.6	871	2	BF675225	C	209	15	83.3	293	1	AW068093
C	137	15.4	85.6	872	6	CD515994	C	210	15	83.3	298	1	AB393561
C	138	15.4	85.6	876	5	BUL189739	C	211	15	83.3	305	1	AA502726
C	139	15.4	85.6	881	5	BK361165	C	212	15	83.3	311	3	BP283595
C	140	15.4	85.6	885	3	BQ232885	C	213	15	83.3	314	3	BM768553
C	141	15.4	85.6	886	8	BX416924	C	214	15	83.3	320	1	AW161667
C	142	15.4	85.6	911	5	BK328031	C	215	15	83.3	321	1	AW516657
C	143	15.4	85.6	924	2	BB540523	C	216	15	83.3	322	1	AW1278707
C	144	15.4	85.6	931	10	CW294982	C	217	15	83.3	323	5	BX737513
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C	146	15.4	85.6	936	2	BP165108	C	219	15	83.3	330	1	AA06454
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C	148	15.4	85.6	951	5	BQ80107	C	221	15	83.3	337	8	T40539
C	149	15.4	85.6	973	10	CZ2921167	C	222	15	83.3	338	1	AA182773
C	150	15.4	85.6	1000	10	CG3355229	C	223	15	83.3	338	1	AA479918
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C	152	15.4	85.6	1024	6	BQ202996	C	225	15	83.3	339	1	BE080524
C	153	15.4	85.6	1046	6	CB961670	C	226	15	83.3	340	1	AI077915
C	154	15.4	85.6	1096	1	AL515292	C	227	15	83.3	342	2	BF39440
C	155	15.4	85.6	1120	1	AL531514	C	228	15	83.3	348	1	AI086019
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C	157	15.4	85.6	1200	1	DN685116	C	230	15	83.3	348	1	AA303091
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C	159	15.4	85.6	14053	4	AK051544	C	232	15	83.3	355	1	AA6151534
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C	161	15.4	85.6	1428	1	AA28531	C	234	15	83.3	362	2	BG94684
C	162	15.4	85.6	1467	8	W42749	C	235	15	83.3	363	1	AA953293
C	163	15.4	85.6	150	1	A1128833	C	236	15	83.3	363	1	AA84009
C	164	15.4	85.6	153	6	CD177653	C	237	15	83.3	364	1	AW173294
C	165	15.4	85.6	159	1	AA86024	C	238	15	83.3	364	1	AW665209
C	166	15.4	85.6	159	1	AA327953	C	239	15	83.3	367	1	BG752518
C	167	15.4	85.6	169	1	AA897749	C	240	15	83.3	371	2	BP058492
C	168	15.4	85.6	172	7	CN260722	C	241	15	83.3	371	8	W42436

FEATURES	ORGANISM
Source	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
	REFERENCE 1 (bases 1 to 656)
	Araakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Itoh,M., Kawai,J., Kono,H., Kouza,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Ochiai,T., Saito,R., Sakai,K., Sano,H., Sasaki,D., Shinoda,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse EG5 (Araakawa,T., et al. 2001)
	TITLE JOURNAL COMMENT Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory: Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) The Institute of Physical and Chemical Research (RIKEN) Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-reseqc.riken.jp, URL: http://genome.gsc.riken.jp/
	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. <i>Genome Res.</i> . 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Osawa,K., Tanaka,T., Matsumura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A., and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. <i>Genome Res.</i> . 10 (11), 1757-1771 (2000) Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. <i>Genome Res.</i> . 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fuhkada,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y. Mapping of 1932 mouse cDNAs on mouse chromosomes. <i>J. Struct. Funct. Genomics</i> 2 pre, 172-L86 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. Location/Qualifiers
	e 1. .656 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10990" /clone="8830124F20" /sex="male" /tissue_type="bone" /dev_stage="adult" /lab_host="DHIOB" /clone lib="RICKEN full-length enriched, adult male bone" /note="Site 1: Sali; Site 2: BamHI; cDNA library was
	CE1356935 qk21d07.x AM070134 x11b08.x BG231838 nf31f02. BR388515 BR388515 AA550930 n186d11.s BN92970 UT-H-D01 AT1762657 wh8f05.x BX413818 BX413818 BG11052 602278983 AT052485 ox19f12.x CR612702 full1-leng BX421021 BX421021 CN192912 CN192912 PEDH1911 PE DH1911 AT222030 qb01904.x AA69495 z243c10.s AI091825 qas8c05.s AQ118929 HS 3011-B AA80590 ob7903.s AI07617 Q9QD80.X AI018107 ot91d08.s AA464265 zx81d10.s AT29967 q242b02.x AW26343 xq47909.x AQ118929 HS 3011-B AA80590 ob7903.s AA523728 n931b03.s BU730512 UT-E-C11 AI29967 q242b02.x AW26343 xq47909.x AQ118929 HS 3011-B AA80590 ob7903.s AI080097 o236a07.x CP382840 lac68h01. AI249324 qh70e01.x AI354517 qh46902.x N33480 yy22d10.s1 AA065082 zml13a04.s AI744302 tr09a01.x CN137433 OX11-57.F0 C278 15 83.3 428 7 CN137433 C279 15 83.3 429 1 AA999919 C280 15 83.3 432 8 W86074 zd91c09.s1 C281 15 83.3 433 1 AA72811 ah87f02.s C282 15 83.3 433 1 AA548118 nj14908.s C283 15 83.3 433 3 BM709842 UI-E-C01. C284 15 83.3 433 1 AI445510 t330a09.x C285 15 83.3 436 2 BG223171 nsh65c02. C286 15 83.3 437 1 AA458972 zx88g07.s C287 15 83.3 440 8 RS4623 YJ49509.s1 C288 15 83.3 442 5 BU935555 AGENCOURT CE428666 tigr-gbs- AI446090 t33f09.x AI1032723 ox11c04.x AI300503 q019c10.x AA291557 zt45e04.s AA533309 n165g04.s AI168496 ou64h05.s AI168496 wh19h01.x AT1761144 wh19h01.x N26709 yk11c12.s1 BU734199 UT-E-C01- A1243467 qh19e11.x A1243467 1 BU508676 AGENCOURT

modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Query Match Best Local Similarity 100.0%; Score 18; DB 2; Length 656; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGGACCTTAGAGGCAAG 18

Db 345 CGGACCTTAGAGGCAAG 362

RESULT 2

BY27643

LOCUS BY727643

DEFINITION RIKEN full-length enriched, 6 days neonate medulla oblongata Mus musculus cDNA clone B73002D01 5', mRNA sequence.

ACCESSION BY727643

VERSION BY727643.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Bukaytoya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathini; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 674)

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Niakido,I., Otao,N., Saito,R., Suzuki,H., Yamamoto,I., Kiyobashi,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Built,C., Hume,D.R., Quackenbush,J., Schriml,L.M., Kampi,A., Matsuda,H., Batyalov,S., Beselj,K.W., Blake,J.A., Bradt,D., Brusic,V., Chotila,C., Corbani,L.E., McKenzie,D., Dalla,E., Dragani,T.A., Fletcher,C.P., Forrest,A., Frazer,K.S., Gasterland,T., Gariboldi,M., Giassi,C., Gozicki,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Kedierski,R.M., King,B.L., Konagaya,A., Kawaji,H., Kawasawa,Y., Kedierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyon,P.A., Maglott,D.R., Maltis,L., Marchionni,L., Mikiti,H., Nagashima,T., Numata,K., Okido,T., Pavani,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pilai,R., Pontius,J.U., Qi,D., Ramachandran,S., Reeder,J.C., Reed,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultan,R., Takanaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wallstedt,C., Wang,Y., Watabane,Y., Wells,C., Wilming,L.G., Wyrshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,K., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hasizume,M., Imoriaki,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sasaki,D., Shibata,K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E., and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-rep@gsc.riken.jp URL:<http://genome.gsc.riken.jp/>

PUBLISHED 12466051

JOURNAL

ORIGIN

REFERENCE

AUTHORS

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1755-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (12), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

RESULT 3

BB613725

LOCUS BB613725

DEFINITION RIKEN full-length enriched, 0 day neonate head Mus musculus cDNA clone 481413M17 5', mRNA sequence.

ACCESSION BB613725

VERSION BB613725.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

Bukaytoya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathini; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 688)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Steinbock-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-533-9222, Fax: 81-45-503-9116)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/

FEATURES
source

Location/Qualifiers

1. -2751

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:9830134F20"
/db_xref="taxon:10090"
/clone="9830134F20"
/sex="male"
/tissue type="bone"
/clone Lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. -2751

/note="kinase suppressor of ras (MGI:105051, GB|NM_013571, evidence: BLASTN, 100%, match=1985)"

ORIGIN

Query Match 100.0%; Score 18; DB 4; Length 2751;
Best Local Similarity 100.0%; Prd. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACCTAGAGCAAG 18
345 CGAACCTAGAGCAAG 362

db

RESULT 5
CK370327/c
LOCUS CK370327 317 bp mRNA linear EST 23-DEC-2003
DEFINITION zmrw005_0a10-002-b11.80
ACCESSION zmrw005
VERSION CK370327
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Spermato phyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
REFERENCE 1 (bases 1 to 317)
AUTHORS Bohnerth,H., Sharp,R.E., Springer,G.K., Poroyko,V., Frederickson,M.,
Sharp,L.G., Spollen,W.G., Ries,J., Guillen,A., Khamati,A.,
Topinka,C., Davis,G.E., Schachman,D., Wu,Y. and Nguyen,H.T.
TITLE NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root
JOURNAL Unpublished (2003)
COMMENT Contact: Hans Bohnerth
University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5474
Fax: 217-333-5574
Email: bohnerth@life.uiuc.edu
POLY=A
FEATURES source
Location/Qualifiers
1. -317
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone Lib="zmrw005"
/note="Library zmrw005 consists of the same cDNA

material as library zmrw00 (described below) but was sequenced from the 5' prime end. The sequence identifier uses the ".80" suffix because the library tag was at the 3' prime end and thus not identified. Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Bark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high (-0.03 MPa) or low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrw05 and zmrw48) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohnerth (University of Illinois-UC). Total RNA was extracted by the hot phenol method (Plant Molecular Biology manual, DS: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/A280). Poly(A)+mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dt) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dt) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (Root Segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were digested with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested PBS II SK(+) phagemid vector (Stratagene) and electroporated into E. coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw05: 3.37 x 106; zmrw48: 4.87 x 106; zmrw00: 3 x 106. The background of empty clones was less than 1%. Inserts ranged from ~0.5 kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30°C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw05: 2.0x107; zmrw48: 4.2x107; zmrw00: 1.1x107. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5 kb to 2.5 kb. (1) Sharp, R. E.; Slik, W. K.; Hsiao, T. C. Growth of the Maize Primary Root at Low Water Potentials I: Spatial Distribution of Expansive Growth. Plant Physiology (Rockville), 87(1), 1988, 50-57. (2) Spollen, W. G.; LeNoble, M. B.; Samuel, T. D.; Bernstein, N.; Sharp, R. E. Abscisic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville), 122(3), March,

2000. 967-976. Score 16.4; DB 7; Length 317;
TAG TISSUE=Not found
TAG_SEQ=Not found"

ORIGIN

Query Match 91.1%; Score 16.4; DB 7; Length 317;
Best Local Similarity 94.4%; Pred. No. 1.2e-03; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGGACCTAGGGCAAG 18
Db 41 CGGACCTAGGGCAAG 24

RESULT

RESULT 6
CF633642 CF633642 370 bp mRNA linear EST 02-OCT-2003
LOCUS zmrw000 0A10-002-b11.s0 zmrw000 Zea mays cDNA 3', mRNA sequence.
DEFINITION zmrw000 0A10-002-b11.s0 zmrw000 Zea mays cDNA 3', mRNA sequence.
ACCESSION CF633642
VERSION CF633642.1
KEYWORDS EST
SOURCE zea mays
ORGANISM zea mays

Bukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCD
REFERENCE 1 (bases 1 to 370)
Bohnert,H., Sharp,R.E., Springer,G.K., Poroyko,V., Fredricksen,M.,
Sharp,L.G., Spoollen,W.G., Ries,J., Guillen,A., Khambati,A.,
Topinka,C., Davis,G.E., Schachman,D., Wu,Y., and Nguyen,H.T.,
NSP Grant DBI-0211842; Functional Genomics of Root Growth and Root
Signaling Under Drought
JOURNAL Unpublished (2003)
COMMENT Contact: Hans Bohnert
University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohnert@life.uiuc.edu
POLY(A)=No

FEATURES
source
1. .370
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="Taxon:4577"
/clone_line="zmrw00".
/note="Samples were collected in Robert E. Sharp's lab
(University of Missouri-Columbia) to construct three
normalized cDNA libraries. Dark-grown maize seedlings with
primary root 12-20 mm in length were transplanted to high
(-0.03 MPa) or low water potential (-1.6 MPa) vermiculite,
and harvested at 5 h and 48 h after transplanting. About
1,000 roots were used for each of the low water potential
libraries (zmrw05 and zmrw48) while 500 roots were
combined from each of the time points at high water
potential (zmrw00). Each root was divided into 4 segments
(distances are from the junction of the root apex and root
cap); segment 1, 0-3 mm plus the root cap; segment 2, 3-7
mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details
of conditions see [1] with minor modifications as in
(2)). The three normalized cDNA libraries were constructed
in the lab of Hans Bohnert (University of Illinois-UC).
Total RNA was extracted by the 'hot Phenol' method (Plant
Molecular Biology manual D5: 1-13, 2nd ed., 1997). This
method worked in eliminating carbohydrate material present
in the root tips. The integrity of the RNA was verified by
denaturing agarose gels and spectrophotometry (ratio
A260/280). Poly(A)-mRNA was isolated twice from total RNA
using the Oligoex Direct mRNA kit (Qiagen). Poly(A)+ mRNA
was converted to double-stranded cDNA and tagged by using
modified Oligo(dT) primers. One of 4 sequence tags
corresponding to a different segment of the root was added
to the 3'-end of the modified Oligo(dT) primers, including

a NotI site and used to reverse transcribe the
segment-specific mRNA into cDNAs. Each library contains
all four tags. A suffix (s1, s2, s3, or s4) has been added
to each sequence identifier to designate which region of
the root (Root segment 1, 2, 3, or 4) the sequence was
found in based on the identification of the tag. A suffix
of s0 indicates that the sequence tag, and hence the
source segment, could not be identified. The double
stranded cDNAs were size-selected (>450 bp). Size selected
cDNAs were adaptored with EcoRI adaptors at both ends, and
then digested with NotI. The cDNA was directionally cloned
into EcoRI-NotI digested PBS II SK(+) phagemid vector
(Stratagene) and electroporated into E. coli DH10B. The
total number of white colony forming units (cfu) in the
primary libraries before amplification was as follows:
zmrw05: 3.37 x 106; zmrw48: 4.87 x 106; zmrw00: 3 x
106. The background of empty clones was less than 1%.
Inserts ranged from ~0.5kb to >2.5 kb, as determined by
PCR. Plasmid DNA from the primary libraries was then was
converted to single-stranded circles and used as a
template for PCR amplification using the T7 and T3 priming
products that flank the cloned cDNA inserts. The purified PCR
products, representing the entire cDNA population cloned
in each library, were used as a driver for normalization.
Hybridization between the single-stranded library and the
PCR products was carried out for 44 hours at 30°C.
Non-hybridized single-stranded DNA circles were separated
from hybridized DNA rendered partially double-stranded and
electroporated into DH10B. The total number of clones with
insert was: zmrw05: 2.0x107; zmrw48: 4.2x107; zmrw00:
1.1x107. The background of empty clones was less than 2%.
Insert size, determined by PCR of the entire library,
ranged from 0.5kb to 2.5kb. (1) Sharp R.E.; Silk W.K.; Heiao
T.C. Growth of the Maize Primary Root at Low Water
Potentials I. Spatial Distribution of Expansive Growth.
Plant Physiology (Rockville). 87(1). 1988. 50-57. (2)
Spoollen W.G.; LeNoble M.B.; Samuels T.D.; Bernstein N.; Sharp
R.E. Abscisic acid accumulation maintains maize primary
root elongation at low water potentials by restricting
ethylene production. Plant Physiology (Rockville). 122(3).
March, 2000. 967-976.

TAG TISSUE=Not found
TAG_SEQ=Not found"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 370;
Best Local Similarity 94.4%; Pred. No. 1.2e-03; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGACCTAGGGCAAG 18

Db 255 CGGACCTAGGGCAAG 272

RESULT

RESULT 7

BB17998/C

LOCUS BB17998

DEFINITION PMI-HT0790-250600-001-a09 HT0790 Homo sapiens cDNA, mRNA sequence.

ACCESSION BB17998

VERSION BB17998.1

EST

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchopteglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 510)
Dias Neto,F., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.J., Zago,M.A., Bordim,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,I.P., de Souza,S.J. and
Simpson,A.J.

/clone_libr="NIHCD_XGC_Fab"
 /note="Organ: fat body; Vector: pExpress-1; Site_1: EcoRV;
 Site_2: NotI; cDNA was primed using oligo(dT) primer;
 5'-pGACTGATGTCAGATGCCGAGGCCGCT(T_n)₂₅₋₃, and cloned into
 the EcoRV/NotI sites of pExpress-1. Site-selection 1.2kb
 resulted in an average insert size of 1.8kb. This is a
 primary library (normalized library size is NIHCD XGC Fabn) and
 was constructed by Express Genomics (Frederick, MD). Note:
 this is a (<http://cgx.ncbi.nih.gov/>) Xenopus Gene
 Collection library."

Invitrogen pCMVsport6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTCCTTAAACGAG CGCCCGCCCTTTTTTTTT 3'. CDNA were ligated to SallI adapter (5'-TCGACGACGGCTGC and 5'-Cggacgcggc) digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SallI digested pCMVsport6 vector."

ORIGIN

Quare

RESULT 11

RESULT 10
 CX910994
 LOCUS JGI_CANN2676 fwd NIH_XGC_tripe4 mRNA linear EST 04-FEB-2005
 DEFINITION IMAGE:7688136 5', mRNA sequence.
 ACCESSION CX910994
 VERSION CX910994.1
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis

LOCUS DT058319 875 bp mRNA linear EST 11-AUG-2005
DEFINITION AGENTC1T 55953048 NICHD_XGC_Fab Xenopus laevis cDNA clone
IMAGE:80169448 3', mRNA sequence.
ACCESSION DT058319
VERSION DT058319.1 GI:72358668
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae: Xenopus: Xenopus

Xenopus tropicalis (western clawed frog)

Amphibia; **Batrachia;** **Anura;** **Mesobatrachia;** **Pipoidea;** **Pipidae;** **Xenodermidae;** **Xenopus;**

REFERENCE	Bukharyova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Silurana.
AUTHORS	Richardson, P., Lucas, S., Rothsar, D., Detter, J.C., Ng, D.C., Brokstein, P. and Lindquist, B.A.
TITLE	DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL	Unpublished (2004)
COMMENT	Other ESTs: JGI:CLAN2676-rev Contact: Richard.P.Brokstein@jgi.doe.gov

REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC <http://mgcc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniel S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-1@mail.nih.gov

DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 295 5600
Fax: 925 296 5710
Email: cDNA@jgi-doe.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley)
<http://tropicalis.berkeley.edu/home/>
cDNA library Preparation: DOE Joint Genome Institute:
<http://www.Jgi.doe.gov>
DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
Clone Distribution: I.M.A.G.E. Consortium/LINL:
<http://image.llnl.gov>

Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CNA 0025 row: h column: 22
High quality sequence stop: 752.

FEATURES
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organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="LXON:83955"
/clone="IMAGE:8069448"
/lab_host="DH10B Toda"
/clone_id="NICH_XGC_Fab"
/note="Organ: rat body; Vector: pExpress-1; Site_1: BcORV;
 Site 2: NECI; cDNA was primed using oligo-dT primer:
CDNA LIBRARY PREPARATION: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)
DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/L1NL at:
<http://image.llnl.gov>
 Plate: L1NL17342 row: d column: 22
 High quality sequence start: 479
 High quality sequence stop: 795.
location/Qualifiers
 location

FEATURES	LOCATION/QUALIFIERS
SOURCE	1. -817

/dev/stage="Adult"
lab_host="ElectroMAX DH10B"
clone_lib="NIH_XCC_tropie"
note="Vector: pEWSport6; Site_1: SalI; Site_2: NotI;
This library was made from dT primed cDNA and cloned into

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsr@mail.nih.gov
COPYRIGHT CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA LIBRARY Arrayed by: Greg Lennon, Ph.D.
DNA SEQUENCING Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bioprj/image/image.html
Insert Length: 639 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 431.

FEATURES Location/Qualifiers

Source

1. . 538

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/codon="IMAGE:189062"
/sex="male"
/lab_host="DNA0B"
/clone_lib="Soares testis_NHT"
/note="Vector: pRT3D Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer 15' TGTCTACCATCTGAGTCGGAGCGGCCCAATTTTTTTTTTT 3'.
Double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization to Cot5 and was constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN

Query Match 88.9%; Score 16; DB 1; length 538;
 Best Local Similarity 100.0%; Pred. No. 2e+03; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACCTAGGGCAA 17

Db 528 GGACCTAGGGCAA 513

RESULT 17
 AG498153 AG498153 769 bp DNA linear GSS 22-DEC-2004
LOCUS Mus musculus molossinus DNA, clone:MSMg01-397021.T7, genomic survey
DEFINITION sequence.

ACCESSION AG498153
VERSION AC498153.1
KEYWORDS GSS.

SOURCE Mus musculus molossinus (Japanese wild mouse)

ORGANISM Mus musculus molossinus (Japanese wild mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Cattarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 123)

TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
COMMENT Unpublished (1997)
CONTACT Robert Strausberg, Ph.D.
Email: cgapsr@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Bomer-Buch, M.D., Ph.D.

CDNA LIBRARY CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 104.

FEATURES Location/Qualifiers

Source

1. .123

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

JOURNAL Genome Res. 14 (12), 2439-2447 (2004)

PUBLISHER 15574823 (bases 1 to 769)

REFERENCE Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

AUTHORS Direct Submission
TITLE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp; URL:<http://hgp.gsc.riken.go.jp/>); Tel:81-45-530-9111, Fax:81-45-531-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@tc.riken.jp). Tsukuba Institute, Bio Resource Center, Research (RIKEN) 3-1-1, Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
E-mail: abe@tc.riken.jp

PRIMERS Sequencing : T7

LIBRARY Vector : PBACE3.6

R.Site 1 : EcorI

R.Site 2 : EcoRI.

FEATURES Location/Qualifiers

Source

1. .769

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/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57436"
/clone="MSMg01-397021.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_id="MSMg01 Mouse Male BAC Library"
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ORIGIN

Query Match 88.9%; Score 16; DB 10; Length 769;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACCTAGGGCAA 18

Db 160 GACCTAGGGCAA 175

RESULT 18
 BE03972 BE03972 123 bp mRNA linear EST 04-AUG-2000
LOCUS BB503972 BB503972.x1 NCI_CGAP_Lu24 Homo Sapiens cDNA clone IMAGE:3211756 3,
DEFINITION mRNA Sequence.

ACCESSION BB503972
VERSION BB503972.1
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Cattarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 123)

TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
COMMENT Unpublished (1997)
CONTACT Robert Strausberg, Ph.D.
Email: cgapsr@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Bomer-Buch, M.D., Ph.D.

CDNA LIBRARY CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 104.

FEATURES Location/Qualifiers

Source

1. .123

```
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp; URL:<http://hgp.gsc.riken.go.jp/>); Tel:81-45-530-9111, Fax:81-45-531-9170)

Query Match 85.6%; Score 15.4; DB 1; Length 143;
Best Local Similarity 94.1%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN Soares and M. Fatima Bonaldo.

Query Match 85.6%; Score 15.4; DB 2; Length 123;
Best Local Similarity 94.1%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGGCAAG 18
Db 51 GGACCTAGGCCAAG 67

RESULT 19

AI349272/C

LOCUS AI349272 143 bp mRNA linear EST 16-FEB-1999
ta75c07.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2049900 3',
mRNA sequence.

ACCESSION AI349272

VERSION .AI349272.1 GI:4086478

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgbps-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquiu, M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kizman, Ph.D., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbmap/image/Image.html
Seq primer: -40m13 fwd. BT from Amersham
High quality sequence Sop: 142.
Location/Qualifiers

FEATURES source

I..170

/organism="Homo sapiens"
/mol-type="mRNA"
/clone="IMAGE:1202810"
/sex="Male"
/dev-stage="45 years old"
/lab-host="DHIOB"
/clone-lib="NCI_CGAP_Pr3"
/note="Vector: PAM10; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adapter-specific primer, and the resulting PCR product subcloned into PAM10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Kizman."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; Length 170;
Best Local Similarity 94.1%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACCTAGGCAAG 18
Db 65 GGACCTAGGCCAAG 81

RESULT 21

AA234751.

LOCUS AA234751

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DEFINITION	z838c05_s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:687464	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
ACCESSION	AA234751	1 (bases 1 to 205)
VERSION	AA234751.1	GI:1859468
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE		
AUTHORS	Homo sapiens (human)	
JOURNAL		
COMMENT		
TITLE		
COMMENT		
FEATURES		
source		
Query Match	85.6%; Score 15.4; DB 1; Length 177;	
Best Local Similarity	94.1%; Pred. No. 3.8e+03;	
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	2 GGACCCCTAGAGGCCAAG 18	
Db	53 GGACCCCTAGAGGCCAAG 69	
ORIGIN		
RESULT 22		
AC109443/c	At099443 At099443 205 bp mla mRNA linear EST 20-AUG-1998	
DEFINITION	u620f06_x1 Sugano mouse liver mla Mus musculus cDNA clone IMAGE:1431891 3' similar to SW:ALBU_RAT P02770 SERUM ALBUMIN PRECURSOR. [1] ; mRNA sequence.	
ACCESSION	AC109443	
VERSION	AC109443.1	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Hominidae; Homo	
REFERENCE	1 (bases 1 to 215)	
FEATURES		
source		
Query Match	85.6%; Score 15.4; DB 1; Length 177;	
Best Local Similarity	94.1%; Pred. No. 3.8e+03;	
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 CGGACCCCTAGAGGCCAAG 17	
Db	27 CGGTCCCCTAGAGGCCAAG 11	
ORIGIN		
RESULT 23		
BI493189	BI493189 BI493189 215 bp mRNA linear EST 28-AUG-2001	
LOCUS	BI493189	
DEFINITION	ds98e07.w1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:254029 3', mRNA sequence.	
ACCESSION	BI493189	
VERSION	BI493189_1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE		
FEATURES		
source		
Query Match	85.6%; Score 15.4; DB 1; Length 205;	
Best Local Similarity	94.1%; Pred. No. 3.8e+03;	
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 CGGACCCCTAGAGGCCAAG 17	
Db	27 CGGTCCCCTAGAGGCCAAG 11	
ORIGIN		

AUTHORS	Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.	Tel: 301 838 0200 Fax: 301 838 0208 Email: szxiao@tigr.org
TITLE	Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening	Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Peter de Jong
JOURNAL	Genomics 23, 42-50 (1994)	Resources (http://www.tigr.org). Clones may be purchased from BACPAC Page: http://www.chori.org/bacpac/orderingframe.htm . BAC end Plate: 236 row: H column: 6
PUBLISHED	7829101	Seq primer: SP6
COMMENT	Contact: Morton, C. C. Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology Brigham and Women's Hospital 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA Tel: 617 732 7980 Fax: 617 738 6996	Class: BAC ends. Location/Qualifiers
FEATURES	source	1..215 'organism="Homo sapiens"' 'mol_type="mRNA"' 'db_xref="taxon:9606"' 'clone="IMAGE:2540629"' 'tissue_type="cochlea"' 'dev_stage="16-22 week fetus"' 'lab_host="SDR cells (kanamycin resistant)"' 'clone_lib="Morton Fetal Cochlea"' 'notes="Organ: ear; Vector: pBluescript SK-' Site 1: ECORI; Site 2: XbaI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: Oligo dT. Fetal cochlea, normal. 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR vector. Library constructed by N. Robertson, C. Morton. sequence: 5' CTGGAGTTTTTTTTTTT 3'"
ORIGIN		Query Match Score 15.4; DB 3; Length 215; Best Local Similarity 94.1%; Pred. No. 3.9e+03; Mismatches 0; Indels 0; Gaps 0;
QY	2 GAGCCTAGAGCAAG 18	Query Match Score 15.4; DB 9; Length 241; Best Local Similarity 94.1%; Pred. No. 3.9e+03; Mismatches 0; Indels 0; Gaps 0;
Db	28 GGACCTAGAGCCAG 44	LOCUS BI493190/c DEFINITION df98e07_Y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2540629 5', mRNA sequence. ACCESSION BI493190 VERSION BI493190_1 GI:15332534 KEYWORDS EST. SOURCE ORGANISM Homo sapiens (human)
RESULT	24	Query Match Score 15.4; DB 9; Length 241; Best Local Similarity 94.1%; Pred. No. 3.9e+03; Mismatches 0; Indels 0; Gaps 0;
BH084942/c	BH084942	LOCUS BH084942 241 bp DNA linear GSS 18-JUL-2001 DEFINITION RPCI-24-236H6_TV RPCI-24 Mus musculus genomic clone RPCI-24-236H6, genomic survey sequence. ACCESSION BH084942 VERSION BH084942.1 GI:14904539 KEYWORDS GSS. SOURCE ORGANISM Mus musculus (house mouse)
REFERENCE	1 ('bases 1 to 258)	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.	TITLE Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
JOURNAL		JOURNAL COMMENT
PUBLISHED	7829101	Contact: Morton, C. C. Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology Brigham and Women's Hospital 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA Tel: 617 732 7980 Fax: 617 738 6996 Email: cmorton@bwh.harvard.edu
REFERENCE	1 ('bases 1 to 241)	DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NIHSC; see http://www.nisc.nih.gov) This clone is available royalty-free through LInk; contact the IMAGE Consortium (http://www.image.lnl.gov) for further information.
AUTHORS	Zhao,S., Nieman,W., Malek,J., Shatsman,S., Akintret,B., Levins,M., Tsedaye,G., Geer,K., Krolik,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.	Plate: 11AM6328 row: I column: 14
JOURNAL	Unpublished (1999)	Seq primer: M3KPL reverse primer (A81).
COMMENT	Other_GSS: RPCI-24-236H6_TV Contact: Shayning Zhao Department of Eukaryotic Genomics The Institute for Genetic Research 9712 Medical Center Dr., Rockville, MD 20850, USA	FEATURES Location/Qualifiers

Source

1. -258
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540629"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_Lib=Morton Fetal Cochlea
 /note="Organ: ear; Vector: pBluescript SK+; Site 1: ECOLI;
 Site 2: XbaI; Reference: Genomics 23, 42-50. (1994) Cloned
 unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
 37% of inserts 0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZIP
 XR vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GATTCGCAAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTT 3'

ORIGIN

Query Match 85.6%; Score 15.4; DB 2; length 288;
 Best Local Similarity 94.1%; Pred. No. 3. 9e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGACCTAGAGGAAG 18
 Db 77 GGACCTAGAGGAAG 61

QY

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

Tissue procurement

Ph.D.

DNA Library Preparation

CDNA Library Arrayed

DNA Sequencing by

Clone distribution

NCT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLM at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m3 fwd ET from Amersham.

Location/Qualifiers

source

FEATURES

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1266073"

tissue_type="alveolar rhabdomyosarcoma"

lab_host="DH10B"

clone_Lib="NCI_CGAP_Al1v2"

note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; length 295;

Best Local Similarity 94.1%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

Tissue procurement

Ph.D.

DNA Library Preparation

CDNA Library Arrayed

DNA Sequencing by

Clone distribution

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www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m3 fwd ET from Amersham.

Location/Qualifiers

source

FEATURES

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1266073"

tissue_type="alveolar rhabdomyosarcoma"

lab_host="DH10B"

clone_Lib="NCI_CGAP_Al1v2"

note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; length 295;

Best Local Similarity 94.1%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY

REFERENCE

AUTHORS

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JOURNAL

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www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m3 fwd ET from Amersham.

Location/Qualifiers

source

FEATURES

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1266073"

tissue_type="alveolar rhabdomyosarcoma"

lab_host="DH10B"

clone_Lib="NCI_CGAP_Al1v2"

note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; length 295;

Best Local Similarity 94.1%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY

REFERENCE

AUTHORS

TITLE

JOURNAL

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DNA Library Preparation

CDNA Library Arrayed

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Clone distribution

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www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m3 fwd ET from Amersham.

Location/Qualifiers

source

FEATURES

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1266073"

tissue_type="alveolar rhabdomyosarcoma"

lab_host="DH10B"

clone_Lib="NCI_CGAP_Al1v2"

note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; length 295;

Best Local Similarity 94.1%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

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Ph.D.

DNA Library Preparation

CDNA Library Arrayed

DNA Sequencing by

Clone distribution

NCT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLM at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m3 fwd ET from Amersham.

Location/Qualifiers

source

FEATURES

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1266073"

tissue_type="alveolar rhabdomyosarcoma"

lab_host="DH10B"

clone_Lib="NCI_CGAP_Al1v2"

note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; length 295;

Best Local Similarity 94.1%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY

REFERENCE

AUTHORS

TITLE

JOURNAL

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Ph.D.

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CDNA Library Arrayed

DNA Sequencing by

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www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m3 fwd ET from Amersham.

Location/Qualifiers

source

FEATURES

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1266073"

tissue_type="alveolar rhabdomyosarcoma"

lab_host="DH10B"

clone_Lib="NCI_CGAP_Al1v2"

note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; length 295;

Best Local Similarity 94.1%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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CDNA Library Arrayed

DNA Sequencing by

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www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m3 fwd ET from Amersham.

Location/Qualifiers

source

FEATURES

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1266073"

tissue_type="alveolar rhabdomyosarcoma"

lab_host="DH10B"

clone_Lib="NCI_CGAP_Al1v2"

note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; length 295;

Best Local Similarity 94.1%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

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Ph.D.

DNA Library Preparation

CDNA Library Arrayed

DNA Sequencing by

Clone distribution

NCT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLM at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m3 fwd ET from Amersham.

Location/Qualifiers

source

FEATURES

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:1266073"

tissue_type="alveolar rhabdomyosarcoma"

lab_host="DH10B"

clone_Lib="NCI_CGAP_Al1v2"

note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel. average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 85.6%; Score 15.4; DB 1; length 295;

Best Local Similarity 9

ORGANISM	Homo sapiens	www-bio.llnl.gov/bbrp/image/image.html
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	Possible reversed clone: polyT not found	
REFERENCE	1. (bases 1 to 296)	Seq primer: -40bp from Gibco
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	High quality sequence stop: 301.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov	
FEATURES	Insert Procurement: Lee Heiman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.	
source	cDNA Library Preparation: David B. Krizman, Ph.D.	
	cDNA Library Arrayed by: Greg Lennon, Ph.D.	
	DNA Sequencing by: Washington University Genome Sequencing Center	
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbrp/image/image.html	
	Insert Length: 371 Std Error: 0.00	
	Seq primer: -40m13 fwd. ER from Amersham.	
FEATURES	Location/Qualifiers	
source	1. -296	
	/organism="Homo Sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	{clone="IMAGE:1267125"	
	/tissue_type="alveolar rhabdomyosarcoma"	
	/lab_host="DH10B"	
	/clone_lib="NCI_CGAP_Alv1"	
	/note="vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."	
ORIGIN	Query Match	85.6%; Score 15.4; DB 1; Length 313;
	Best Local Similarity	94.1%; Pred. No. 4e+03; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
	Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2. GAACCTAGGGCAAG 18	
Db	62 GGACCTTAGGGCAAG 78	
RESULT	Query Match	85.6%; Score 15.4; DB 1; Length 313;
29	Best Local Similarity	94.1%; Pred. No. 4e+03; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
LOCUS	BM743265/c	
DEFINITION	K-EST0016364 S4SNUL Homo sapiens cDNA clone S4SNUL-10-E01 5', mRNA sequence.	
VERSION	BM743266	
KEYWORDS	EST.	
SOURCE	BM743266.1 GI:19064595	
ORGANISM	Homo Sapiens (human)	
REFERENCE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homidae; Homo.	
AUTHORS	1. (bases 1 to 326) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.	
TITLE	2IC Frontline Korean EST Project 2001	
JOURNAL	Contact: Kim YS Unpublished (2002)	
COMMENT	Korea Research Institute of Bioscience & Biotechnology 52, Beon-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 10 row: E column: 01 High quality sequence stop: 326.	
FEATURES	Location/Qualifiers	
source	1. -326	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
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	/sex="M"	
	/tissue_type="Stomach"	
	/cell_type="Lymphoblast-like"	
	/cell_line="SNU-1"	
	/lab_host="TOP10"	
	/clone_lib="S4SNUL"	
	/note="Organ: Stomach; Vector: pTZ19RPI; Site 1: EcoRI; Site 2: NciI; The Poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped	
REFERENCE	Email: cgaps-r@mail.nih.gov	
AUTHORS	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The	
TITLE	I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov	

with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okavama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 326;
Best local Similarity 94.1%; Pred. No. 4e+03; OMatches 16;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGACCTAGGGCAAG 18
Db 115 GGACCTAGGGCAAG 99

Search completed: April 15, 2006, 18:51:14
Job time : 3827 secs